

					Glu-204 to Gly-214.				
	955327	877	2180 - 1323	1777	Leu-29 to Arg-34, Glu-45 to Thr-50, Tyr-67 to Arg-73, Pro-83 to Gln-108, Asp-117 to Val-123, Gln-148 to Glu-155.				
499	HWWCL36	955759	509	2 - 676	1409			AR089: 7, AR061: 2 H0657: 1, T0023: 1, L0803: 1, H0521: 1, L0731: 1, S0026: 1 and H0423: 1.	
500	HDTEN41	955895	510	1 - 1464	1410	Pro-1 to Arg-16.		AR089: 17, AR061: 7	19
501	HSDDD20	956046	511	1 - 657	1411	Asp-25 to Glu-38, Ala-98 to Phe-104, Gln-152 to Leu-157.		AR089: 1, AR061: 0 S0028: 3, S0001: 2, H0617: 2, L0361: 2, S0356: 1, S0045: 1, H0619: 1, S0278: 1, H0250: 1, H0231: 1, H0181: 1, S0390: 1 and S0031: 1.	
502	HDPBL08	959377	512	173 - 979	1412			AR061: 2, AR089: 2 H0616: 4, L0758: 4, H0341: 2, S0358: 2, L0438: 2, L0748: 2, L0779: 2, H0265: 1, S0222: 1, H0431: 1, H0013: 1, H0253: 1, S0010: 1, H0428: 1.	

503	HMELJ75	960354	513	114 - 1187	1413	Leu-16 to Phe-21, Thr-69 to Lys-74, Asn-87 to His-92, Thr-126 to Leu-137, Phe-154 to Lys-164, Ala-171 to Asp-178, Ile-192 to Thr-203, Glu-261 to Ser-273.	L0456: 1, H0038: 1, L0151: 1, H0063: 1, H0494: 1, L0767: 1, L0657: 1, S0052: 1, S0152: 1, H0521: 1, L0750: 1, H0707: 1 and H0542: 1.		
							AR061: 4, AR089: 3 S0003: 2, H0591: 2, H0529: 2, L0663: 2, L0750: 2, L0752: 2, L0596: 2, H0171: 1, H0341: 1, H0662: 1, S0420: 1, S0132: 1, H0411: 1, S0222: 1, H0013: 1, H0266: 1, H0428: 1, H0039: 1, H0622: 1, L0483: 1, H0644: 1, H0598: 1, H0040: 1, H0634: 1, L0564: 1, H0280: 1, S0150: 1, L0800: 1, L0764: 1, L0662: 1, L0766: 1, L0529: 1, L0666: 1, H0144: 1, H0660: 1, S0152: 1, H0521: 1, L0779: 1, L0777: 1, L0757: 1, L0758: 1 and H0543: 1.		
504	HT.TCU08	960951	514	27 - 686	1414	Thr-1 to Asp-17.	AR061: 4, AR089: 3		

Lys-38 to Glu-45, Tyr-74 to Arg-79, Ala-90 to Val-95, Phe-124 to Gln-142, Val-180 to His-189.	L0777: 13, L0740: 8, L0759: 5, L0608: 5, H0031: 4, H0042: 3, L0771: 3, L0665: 3, L0748: 3, L0439: 3, L0754: 3, H0024: 2, L0769: 2, L0794: 2, L0766: 2, L0806: 2, L0790: 2, H0521: 2, L0750: 2, L0756: 2, L0758: 2, L0592: 2, H0556: 1, H0159: 1, T0049: 1, H0657: 1, S0007: 1, S0046: 1, H0619: 1, S0222: 1, H0574: 1, H0486: 1, S0346: 1, H0318: 1, H0581: 1, H0052: 1, H0327: 1, H0051: 1, T0010: 1, H0039: 1, L0483: 1, L0143: 1, H0032: 1, H0673: 1, H0090: 1, H0038: 1, T0067: 1, S0038: 1, H0529: 1, L0640: 1, L0763: 1, L0639: 1, L0667: 1, L0764: 1, L0662: 1, L0768: 1, L0523: 1, L0657: 1, L0659: 1, H0144: 1, H0659: 1, H0658: 1.
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								S0328: 1, H0539: 1, S0378: 1, S0028: 1, L0747: 1, L0752: 1, L0753: 1, L0755: 1, L0731: 1, L0596: 1, L0595: 1, H0543: 1 and S0412: 1.			
505	HTOHK41	960955	515	1065 - 151	1415		His-10 to Pro-16.	AR089: 20, AR061: 6 H0265: 2, S0040: 1, H0250: 1 and H0264: 1.			
506	HTKAA03	961002	516	2 - 202	1416		Asn-1 to Thr-9, Thr-40 to Asp-51.	S0300: 1, S0028: 1 and T0047: 1.			
507	HMSGF27	962420	517	3 - 332	1417		Arg-1 to Asp-6, Ala-47 to Pro-58.	AR089: 12, AR061: 8 L0766: 4, H0052: 3, L0662: 3, L0776: 3, L0666: 3, L0665: 3, H0521: 3, H0438: 2, H0581: 2, H0263: 2, H0494: 2, L0763: 2, L0770: 2, L0769: 2, L0649: 2, L0664: 2, L0748: 2, L0439: 2, L0747: 2, S0436: 2, H0265: 1, H0556: 1, S0040: 1, S0444: 1, S0278: 1, H0415: 1, H0403: 1, H0643: 1, S0280: 1, H0575: 1, H0194: 1, H0309: 1, H0545: 1, H0046: 1,			

508	HHFLM17	963511	518	3 - 470	1418	Pro-45 to Pro-52, Asn-79 to Ala-84, Gly-124 to Ser-129.	AR089: 2, AR061: 1 H0619: 1, H0529: 1, L0375: 1 and H0543: 1.	L0157: 1, H0375: 1, L0483: 1, H0553: 1, H0412: 1, H0646: 1, S0002: 1, L0796: 1, L0644: 1, L0764: 1, L0774: 1, L0376: 1, L0806: 1, L0654: 1, L0659: 1, L0383: 1, S0126: 1, H0684: 1, H0435: 1, H0478: 1, S0028: 1, L0751: 1, L0754: 1, L0749: 1, L0750: 1, L0779: 1, L0759: 1, H0543: 1 and H0423: 1.	1p32-p34	120950, 120960, 130500, 133200, 138140, 168360, 171760, 171760, 176100, 176100, 178300, 187040, 230000, 255800, 600101,
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									600650, 600650, 600722, 600722
509	HLICL10	964035	519	3 - 761	1419	Glu-121 to Lys-126, Pro-148 to Lys-154, Thr-181 to Asp-187, Val-208 to Asp-214, Pro-223 to Phe-231, Glu-239 to Lys-245.	AR089: 99, AR061: 59 H0393: 1, S0278: 1, H0643: 1, H0196: 1, H0231: 1, H0200: 1, H0355: 1, S0037: 1, S0027: 1, H0445: 1 and H0423: 1.		
510	HCUAZ04	965585	520	546 - 214	1420	Lys-6 to Phe-11.	AR089: 1, AR061: 0 L0769: 8, L0748: 4, L0759: 4, H0038: 3, L0750: 3, L0755: 3, H0556: 2, S0356: 2, H0574: 2, L0163: 2, L0766: 2, L0776: 2, L0663: 2, L0752: 2, L0731: 2, L0599: 2, H0255: 1, H0306: 1, H0125: 1, S0376: 1, H0580: 1, H0455: 1, H0497: 1, H0331: 1, L0021: 1, H0004: 1, H0618: 1, S0010: 1, H0546: 1, H0545: 1, H0123: 1, H0081: 1, H0578: 1, H0051: 1, H0510: 1, H0188: 1,		

									H0617: 1, H0032: 1, H0169: 1, T0042: 1, L0475: 1, H0560: 1, H0132: 1, L0770: 1, L0372: 1, L0764: 1, L0771: 1, L0774: 1, L0783: 1, L0665: 1, L0438: 1, S0028: 1, L0439: 1, L0740: 1, L0786: 1, L0779: 1, L0757: 1, L0758: 1, L0588: 1, L0605: 1, S0192: 1 and S0276: 1.			
511	HE2SB11	965611	521	103 - 441	1421				AR089: 4, AR061: 1 L0435: 2, H0624: 1, L0717: 1, S0214: 1, L0662: 1, L0766: 1, L0803: 1, S0380: 1, H0555: 1, L0754: 1 and L0756: 1.			
512	HCFLJ17	954723	522	1 - 423	1422	Thr-2 to Gln-9, Glu-19 to Glu-29, Glu-43 to Ser-67.			AR089: 4, AR061: 2 L0758: 7, L0362: 5, S0358: 4, L0766: 4, L0754: 4, H0318: 3, H0551: 3, H0529: 3, L0803: 3, H0519: 3, L0750: 3, L0777: 3, H0423: 3, H0650: 2, H0369: 2, H0575: 2, T0110: 2, S0003: 2,			

	H0268: 2, L0770: 2, L0662: 2, L0375: 2, H0144: 2, S0374: 2, S0152: 2, L0780: 2, L0752: 2, L0731: 2, H0445: 2, L0596: 2, L0605: 2, L0599: 2, L0608: 2, H0543: 2, H0624: 1, H0170: 1, H0657: 1, H0402: 1, S0420: 1, S0360: 1, H0675: 1, S0045: 1, L0717: 1, H0600: 1, H0587: 1, H0497: 1, H0574: 1, H0098: 1, H0037: 1, L0105: 1, S0474: 1, H0581: 1, H0052: 1, H0544: 1, L0471: 1, H0060: 1, H0328: 1, H0622: 1, L0483: 1, L0055: 1, H0598: 1, H0090: 1, H0040: 1, H0413: 1, H0561: 1, L0638: 1, L0667: 1, L0646: 1, L0794: 1, L0774: 1, L0805: 1, L0655: 1, L0527: 1, L0657: 1, L0659: 1, L0526: 1, L0783: 1, L0666: 1, H0520: 1, H0690: 1,	
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513	HLICJ19	966969	523	1 - 321	1423	1778	Glu-14 to Glu-24, Glu-38 to Ser-62, Ala-177 to Ala-198, Glu-235 to Arg-240, His-257 to Lys-374.	H0658: 1, H0660: 1, H0521: 1, H0555: 1, S0028: 1, L0742: 1, L0756: 1, S0192: 1, S0242: 1, S0194: 1 and S0276: 1.		
514	HDPSM18	967483	524	1 - 315	1424	1424	Thr-27 to Asn-33.	AR061: 27, AR089: 6 S0040: 1, H0355: 1, H0328: 1, L0374: 1, L0794: 1, L0766: 1 and S3014: 1.		
515	HMAKJ82	967593	525	1 - 501	1425	1425	Thr-3 to Gly-13, Trp-35 to Glu-40, Ser-51 to His-56.	AR061: 2, AR089: 1 H0556: 1, S0212: 1, H0373: 1, H0553: 1, H0063: 1, H0477: 1, S0152: 1, H0521: 1 and S0026: 1.		

516	HFP1X37	971428	526	1 - 507	1426	Pro-75 to Asp-84, Pro-92 to Pro-101, Arg-161 to Trp-167.	H0549: 2, H0497: 2, H0486: 2, H0052: 2, H0150: 2, L0471: 2, H0181: 2, S0002: 2, H0529: 2, L0517: 2, L0666: 2, H0520: 2, L0757: 2, S0116: 1, S0045: 1, S0278: 1, H0013: 1, L0738: 1, H0050: 1, H0012: 1, H0622: 1, T0023: 1, H0087: 1, T0067: 1, H0494: 1, S0142: 1, S0344: 1, L0763: 1, L0769: 1, L0768: 1, L0803: 1, L0650: 1, L0775: 1, L0805: 1, L0776: 1, L0655: 1, L0657: 1, L0658: 1, L0636: 1, L0384: 1, S0052: 1, H0144: 1, S0374: 1, H0519: 1, S0328: 1, H0696: 1, L0439: 1, L0751: 1, L0754: 1 and L0753: 1.	AR089: 4, AR061: 1, H0583: 1, H0662: 1, S0222: 1, S0049: 1, H0272: 1, H0670: 1, H0521: 1, H0555: 1 and
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517	HHEKP47	974402	527	75 - 527	1427	Ser-1 to Thr-7, Pro-15 to Asp-22, Glu-138 to Ser-143.	S0436: 1. AR089: 1, AR061: 1 H0542: 6, H0637: 3, H0580: 3, H0555: 2, H0592: 1, H0586: 1, H0544: 1, H0546: 1, H0545: 1, H0529: 1, H0703: 1, H0593: 1, H0521: 1 and H0543: 1.	1q32	114208, 114208, 119300, 120620, 120620, 120920, 134370, 134370, 134370, 134580, 145260, 150310, 150310, 179820, 191045, 600105, 600759, 601494, 601975
518	HTPDV62	418671	528	2 - 358	1428		AR061: 7, AR089: 4 H0663: 2, H0069: 2, H0634: 2, H0635: 1, H0618: 1 and H0039: 1.	1q32-q41	114208, 114208, 119300, 120620, 120620, 120920, 134370, 134370, 134370, 134580,

												145260, 150310, 150310, 179820, 191045, 276901, 600105, 600332, 600759, 601494, 601744, 601975
519	HUSAJ73	567234	529	1 - 201	1429					AR061: 8, AR089: 7 S0045: 1, S0046: 1, H0574: 1 and H0268: 1.	5	
520	HSKCI76	747380	530	115 - 414	1430	Phe-12 to Thr-17.				AR061: 6, AR089: 5	5	
521	HCEOX38	881200	531	3 - 386	1431	Met-1 to Ile-23, Asp-85 to Asp-91.				AR089: 2, AR061: 1 H0052: 1 and H0435: 1.	17p13-p12	100710, 138190, 231200, 254210, 262850, 271900, 600179, 600977, 601202, 601777
522	HFICR59	911317	532	2 - 721	1432	Ser-2 to Lys-7, Thr-73 to Ala-86, Gly-108 to Asn-113,				AR089: 1, AR061: 0 L0794: 6, L0598: 2, L0803: 2, L0748: 2,		

523	HPDVO67	911405	533	1 - 645	1433	Ser-184 to Val-190. Glu-1 to Asp-6, Thr-11 to Glu-20, Val-61 to Pro-67, Ala-128 to Leu-136, Gln-141 to Ser-147, Arg-173 to Pro-179.	S0040: 1, S0046: 1, H0431: 1, H0318: 1, L0766: 1, L0606: 1, L0749: 1, L0758: 1 and S0192: 1. AR089: 2, AR061: 2 L0751: 10, L0666: 4, L0743: 3, H0253: 2, H0622: 2, H0670: 2, L0779: 2, H0685: 1, H0181: 1, S0382: 1, L0372: 1, L0646: 1, L0773: 1, L0767: 1, L0768: 1, L0657: 1, L0665: 1, S0374: 1, H0658: 1, L0749: 1, L0777: 1, L0758: 1 and L0593: 1.	19p13.3	108725, 120700, 133171, 136836, 145981, 147141, 164953, 188070, 600957, 601238, 601846, 602216, 602477
524	H2LAD53	952181	534	1 - 360	1434	Glu-1 to Tyr-10, Lys-37 to Leu-44, Glu-66 to Leu-75, Glu-80 to His-91.	AR089: 18, AR061: 13 S0136: 47, L0769: 10, L0439: 7, L0750: 7, H0620: 5, L0776: 5, L0740: 5, L0752: 5, L0509: 4, L0809: 4, L0666: 4, L0748: 4, H0624: 3, H0265: 3, H0341: 3, S0418: 3, L0717: 3, L0764: 3, L0659: 3, L0755: 3, S0026: 3, H0556: 2,		

	S0356: 2, S0358: 2, S0360: 2, H0574: 2, T0060: 2, S0010: 2, H0046: 2, H0510: 2, H0032: 2, H0169: 2, H0413: 2, H0646: 2, L0646: 2, L0766: 2, L0803: 2, L0805: 2, L0665: 2, S0374: 2, H0519: 2, H0659: 2, H0648: 2, S0328: 2, S0378: 2, S0380: 2, S3014: 2, L0756: 2, L0777: 2, L0731: 2, L0758: 2, L0588: 2, L0589: 2, L0594: 2, H0543: 2, H0171: 1, S0040: 1, T0049: 1, L0002: 1, H0657: 1, H0346: 1, H0255: 1, H0664: 1, H0305: 1, H0589: 1, S0376: 1, H0675: 1, S0045: 1, S0046: 1, H0586: 1, H0587: 1, H0333: 1, H0642: 1, H0331: 1, H0632: 1, H0486: 1, H0013: 1, H0427: 1, L0021: 1, H0575: 1, H0590: 1, S0182: 1, H0085: 1, H0596: 1,						
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	H0546: 1, L0157: 1, H0572: 1, H0571: 1, H0024: 1, L0695: 1, H0373: 1, L0163: 1, S6028: 1, H0266: 1, S0003: 1, H0252: 1, T0006: 1, H0166: 1, H0674: 1, S0364: 1, L0455: 1, H0124: 1, H0598: 1, H0400: 1, H0135: 1, H0163: 1, H0038: 1, H0616: 1, H0551: 1, T0067: 1, H0100: 1, T0041: 1, S0448: 1, S0450: 1, H0509: 1, H0647: 1, S0208: 1, L0770: 1, L0637: 1, L0772: 1, L0372: 1, L0800: 1, L0374: 1, L0662: 1, L0388: 1, L0774: 1, L0775: 1, L0375: 1, L0653: 1, L0628: 1, L0513: 1, L0526: 1, L0518: 1, L0382: 1, L0663: 1, L0664: 1, L0565: 1, L0438: 1, H0660: 1, H0666: 1, S0044: 1, S0037: 1, S0206: 1, L0747: 1, L0780: 1, L0753: 1,
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									L0757: 1, L0759: 1, H0445: 1, L0592: 1, L0485: 1, L0608: 1, L0603: 1, L0097: 1 and S0446: 1.		
525	HETLM90	972357	879	672 - 887	1779	Glu-42 to Val-48, Glu-63 to Asp-72.			AR061: 7, AR089: 6 S0404: 7, L0754: 4, L0731: 4, H0046: 3, L0662: 3, H0519: 2, L0439: 2, L0756: 2, L0758: 2, S0242: 2, H0171: 1, L0021: 1, H0194: 1, H0251: 1, L0471: 1, H0057: 1, S6028: 1, H0615: 1, H0063: 1, H0494: 1, L0598: 1, L0520: 1, L0646: 1, L0641: 1, L0794: 1, L0766: 1, L0803: 1, L0666: 1, H0144: 1, S0374: 1, H0690: 1, H0539: 1, S0380: 1, H0696: 1, H0436: 1, L0740: 1, L0755: 1 and S0031: 1.		
		972358	880	848 - 645	1780						
		954181	535	1 - 771	1435	Ile-29 to Gln-36.					
526	HCE5E94	969287	536	270 - 410	1436	Ser-1 to Gly-8, Lys-14 to Pro-21,			AR089: 1 H0619: 5, L0439: 5,		

Set-25 to Cys-33, Pro-37 to Gly-44.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
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		969299	881	889 - 1386	1781	Pro-23 to Trp-28, Pro-35 to Lys-41, Gln-101 to Glu-110, Glu-122 to Gly-129.				
527	HFXXCU55	971074	882	3 - 1097	1782					
		499457	537	183 - 1	1437	Lys-32 to Lys-51.				
528	HEPBV24	513261	538	73 - 393	1438	Glu-24 to His-33.				
529	HFRAU96	527840	539	13 - 363	1439					
530	HTLBD23	527944	540	3 - 413	1440	His-1 to Gly-6, Ser-13 to Phe-18.				
531	HCEBM51	536558	541	3 - 470	1441	Asp-17 to Ala-25.				
532	HSLFF79	609838	542	64 - 741	1442	Phe-132 to Gln-137, Arg-209 to Gly-220.				
		961693	883	866 - 174	1783	Phe-137 to Gln-142,				

533	HKTAB71	661483	543	3 - 398	1443	Arg-214 to Gly-225. Asp-47 to Asn-53, Pro-118 to Thr-132.	AR089: 14, AR061: 4 L0774: 3, L0749: 2, H0239: 1, L0803: 1 and S0378: 1.		
534	HSDIF25	678003	544	36 - 446	1444		AR089: 1, AR061: 0 S0390: 1 and S0260: 1.		
535	HNHHW82	684342	545	3 - 284	1445	Ala-1 to Arg-10, His-15 to Asp-20.	AR089: 11, AR061: 4 S0053: 2 and S0050: 1.		
536	HFATN41	712097	546	259 - 717	1446	Gly-37 to Asp-50.	AR061: 3, AR089: 2 S0300: 1 and H0031: 1.		
537	HFFFG80	733387	547	2 - 478	1447		AR089: 15, AR061: 6 H0050: 1 and H0522: 1.		
538	HSDF73	761657	548	3 - 515	1448		AR061: 139, AR089: 37 S0028: 1 and S0031: 1.		
539	HTLBH79	774422	549	3 - 572	1449		AR054: 22, AR051: 20, AR089: 4, AR061: 3, AR050: 2 L0439: 2, S0358: 1, H0486: 1, H0253: 1, H0593: 1 and H0522: 1.		
540	HBWCD80	777346	550	2 - 868	1450	Glu-11 to Arg-17. Leu-26 to Ser-31, Pro-68 to Lys-82.	AR089: 1, AR061: 0		
541	HSDKI89	786812	551	3 - 521	1451	Asp-8 to Gly-26, Tyr-43 to Ser-49, Ser-137 to Lys-148.	AR061: 1, AR089: 1		

542	HIBDA29	810879	552	2 - 403	1452		AR089: 1, AR061: 1 T0010: 2, H0172: 1, H0100: 1, L0769: 1, L0792: 1, L0745: 1 and L0756: 1.		
543	HLDQU68	825558	553	1 - 429	1453	Trp-10 to Gly-16, Asp-30 to Ala-39, Glu-72 to Ser-87, Asn-112 to Trp-124.	AR061: 9, AR089: 2 H0351: 1 and H0510: 1.		
544	HMUAS41	827510	554	2 - 385	1454	Asn-37 to Gln-42, Thr-56 to Leu-62, Asn-68 to Lys-74.	AR089: 4, AR061: 2 S0007: 3, S0354: 2, H0529: 2, H0645: 1, H0052: 1 and H0039: 1.		
545	HTXOH20	837509	555	1 - 426	1455	Glu-1 to Gly-9, Asn-17 to Lys-22, Asp-30 to Phe-36, Lys-43 to Glu-49, Pro-133 to Lys-142.	AR061: 3, AR089: 2		
546	HSLFG13	847314	556	154 - 705	1456		AR089: 1, AR061: 0 S0028: 1 and S3018: 1.		
547	HDAAS21	850577	557	2 - 724	1457	Leu-26 to Cys-37, Cys-127 to Glu-132.	AR061: 158, AR089: 3 H0497: 2, L0766: 2, L0777: 2, H0589: 1, L0627: 1, L0779: 1, L0759: 1, L0604: 1 and H0506: 1.		
548	HARMH10	852701	558	736 - 146	1458	Gln-1 to Pro-6.	AR089: 9, AR061: 3 H0592: 1, S0150: 1, H0521: 1 and L0740: 1.		
549	HSDAI07	859237	559	72 - 623	1459	Ser-10 to Cys-16.	AR089: 1, AR061: 0		

550	HLDQU41	864996	560	1 - 504	1460	Glu-62 to Arg-69, Ser-140 to Thr-146.	S0126: 2, S0031: 2 and S0045: 1. AR061: 765, AR089: 3 L0803: 10, L0439: 5; L0617: 2, L0774: 2, L0438: 2, L0742: 2, L0747: 2, H0574: 1, H0510: 1, H0038: 1, L0804: 1, L0775: 1, L0789: 1 and L0581: 1.		
551	HJBU06	864997	561	20 - 937	1461	Ser-29 to Ser-38, Ser-63 to Thr-69, Glu-90 to Asp-97, Phe-127 to Glu-135, His-215 to His-229, Asp-245 to Asp-257.	AR089: 4, AR061: 2 H0359: 1 and H0561: 1.		
552	HSLDO63	866332	562	3 - 521	1462	Trp-14 to Asn-30, Val-44 to Leu-50, Leu-116 to Tyr-121, Ser-164 to Thr-172.	AR061: 4, AR089: 4 S0028: 1 and H0542: 1.		
553	HNHAG26	866694	563	251 - 880	1463		AR061: 7, AR089: 2		
554	HGBBC61	867065	564	449 - 3	1464		AR089: 1, AR061: 0 H0416: 1, H0181: 1, H0617: 1 and H0316: 1.		
555	HMAEM27	870252	565	3 - 716	1465		AR089: 88, AR061: 44 H0494: 1, S0144: 1, L0749: 1, L0605: 1 and L0593: 1.		
556	HEBCK42	875541	566	313 - 74	1466	Glu-1 to Lys-6,	AR089: 26, AR061: 9	10q11.1-q24	157640,

557	HELFN03	881180	567	323 - 736	1467	Arg-8 to Met-21, Ser-32 to Ala-37.	Lys-15 to Asp-25.	H0031: 4, S0007: 1 and L0748: 1.	174900, 180250, 186770, 188550, 236730, 271245, 278000, 278000, 600095, 600512, 600835, 601107, 601130, 602082
558	HKIMF95	882308	568	1 - 270	1468			AR089: 2, AR061: 1 H0381: 2, H0617: 2, S0045: 1 and S0044: 1. AR061: 399, AR089: 71 H0069: 1, H0399: 1, S0428: 1, H0698: 1 and H0521: 1.	
559	HTLHE85	883263	569	1 - 663	1469	Tyr-20 to Trp-25, Leu-39 to Ser-44, Asp-62 to Thr-79.		AR089: 18, AR061: 13 H0618: 2, H0013: 1 and H0424: 1.	
560	HTEOE72	886412	570	1 - 675	1470	Thr-2 to Ser-9, Pro-23 to Arg-30, Pro-44 to Arg-49, Ser-62 to Pro-73, Phe-150 to Lys-155.		AR050: 14, AR051: 12, AR054: 10, AR061: 6, AR089: 3 H0038: 2, H0616: 1, S0152: 1 and S0242: 1.	

561	HELBN13	907599	571	318 - 659	1471	Asp-164 to Glu-169, Leu-191 to Val-198.	AR089: 1, AR061: 1 S0045: 1, S0144: 1, S0028: 1 and S0260: 1.			
562	HFJE03	914882	572	1762 - 1052	1472	Pro-11 to Asn-16, Lys-67 to His-75, Gly-145 to Trp-152, Glu-171 to Arg-176, Met-220 to Glu-230.	AR089: 15, AR061: 6 L0766: 3, L0596: 2, S0134: 1, H0327: 1, T0010: 1, H0616: 1, H0551: 1, L0363: 1, L0783: 1, H0520: 1, S0152: 1, H0555: 1, L0748: 1, L0439: 1, S0194: 1, H0423: 1 and H0506: 1.			
563	HABGE01	915743	573	2 - 1276	1473	Leu-39 to Lys-47, Gly-67 to Thr-76, Thr-86 to Thr-96.	AR089: 0, AR061: 0			
564	HWLKM02	917409	574	1012 - 11	1474	Ala-2 to Glu-7, Leu-9 to Pro-17, Pro-30 to Glu-41, Gln-50 to Gly-56.	AR089: 3, AR061: 2 S0358: 5, H0617: 4, H0559: 3, L0804: 2, L0805: 2, H0657: 1, S0007: 1, H0455: 1, H0618: 1, H0546: 1, H0545: 1, H0488: 1, L0637: 1, L0775: 1, L0809: 1, L0789: 1, L0438: 1, L0439: 1, L0752: 1 and L0757: 1.			
565	HOVEB13	917564	575	122 - 904	1475	Gly-27 to Ala-33,	AR089: 5, AR061: 2			

566	HE8UB94	920288	576	187 - 561	1476	Gly-16 to Glu-21.	<p>Leu-45 to Asn-53, Lys-86 to Ala-91, Ala-132 to Arg-137, Lys-174 to Phe-183, Gln-200 to Pro-207, Asp-251 to Gln-256.</p>	<p>L0779: 4, H0428: 3, L0773: 2, L0662: 2, L0659: 2, L0602: 2, L0777: 2, L0596: 2, L0608: 2, H0170: 1, H0580: 1, S0045: 1, T0048: 1, H0052: 1, L0471: 1, H0628: 1, L0770: 1, L0761: 1, L0805: 1, L0653: 1, L0657: 1, L0512: 1, H0682: 1, H0672: 1, L0748: 1, L0740: 1, L0749: 1, L0757: 1, S0031: 1, H0543: 1 and H0677: 1.</p>		
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567	HTHDJ23	921274	577	1368 - 1739	1477	Ser-25 to Lys-30.	AR051: 27, AR050: 26, AR054: 22, AR061: 4, AR089: 4 S0358: 1, H0266: 1,
							S0116: 1, H0341: 1, S0045: 1, S0222: 1, S6014: 1, H0431: 1, H0587: 1, H0331: 1, H0486: 1, H0156: 1, L0021: 1, S0049: 1, H0309: 1, H0046: 1, H0086: 1, H0123: 1, S0388: 1, H0687: 1, H0111: 1, H0598: 1, H0616: 1, H0264: 1, H0561: 1, H0538: 1, S0426: 1, L0637: 1, L0646: 1, L0764: 1, L0521: 1, L0364: 1, L0803: 1, L0775: 1, L0527: 1, L0666: 1, H0144: 1, S0374: 1, H0519: 1, H0690: 1, H0435: 1, H0648: 1, S0330: 1, S0152: 1, L0748: 1, L0751: 1, L0745: 1, L0747: 1, L0731: 1, L0758: 1, H0423: 1, H0422: 1 and S0462: 1.

568	HWHPB72	922580	578	454 - 768	1478	Thr-10 to Val-15, Asp-35 to Leu-41.	AR089: 4, AR061: 3 L0438: 3, S0007: 2, S0134: 1, H0587: 1, H0497: 1, H0123: 1, H0428: 1, H0039: 1, H0551: 1, H0623: 1, H0509: 1, H0435: 1, H0518: 1, L0748: 1 and L0759: 1.		
569	HSQFX64	922581	579	1 - 324	1479	Glu-21 to Ser-27, Glu-74 to Val-88.	AR089: 11, AR061: 6		
570	HDABB84	922582	580	3 - 1760	1480	Leu-58 to Asp-68, Thr-91 to Val-96, Asp-116 to Leu-122, Glu-220 to Ser-226.	AR089: 9, AR061: 1 H0056: 2, H0059: 2, L0800: 2, L0663: 2, L0602: 2, L0747: 2, L0588: 2, L0591: 2, L0592: 2, L0599: 2, H0686: 1, S0360: 1, S0132: 1, H0497: 1, S0280: 1, H0042: 1, S0036: 1, H0634: 1, L0351: 1, H0560: 1, S0448: 1, H0509: 1, H0529: 1, L0764: 1, L0794: 1, L0774: 1, L0775: 1, L0375: 1, L0809: 1, L0666: 1, S0374: 1, L0438: 1,		

									H0547: 1, H0435: 1, H0651: 1, S0380: 1, L0748: 1, L0749: 1, L0779: 1, L0752: 1, L0731: 1, L0759: 1, H0543: 1, H0423: 1 and H0506: 1.			
571	HLHFN83	924110	581	3 - 263	1481				AR089: 14, AR061: 8 H0510: 2, L0595: 2, H0657: 1, H0580: 1, H0619: 1, H0357: 1, H0632: 1, H0013: 1, H0024: 1, H0578: 1, H0591: 1, H0509: 1, L0769: 1, L0804: 1, L0805: 1, L0776: 1, H0521: 1, H0555: 1, L0740: 1, L0749: 1 and H0423: 1.			
572	HPCRR26	926401	582	870 - 253	1482	Asp-10 to Thr-15, Leu-19 to Arg-26, Gly-120 to Asn-125, Lys-131 to Ser-139, Gly-169 to Lys-174, Glu-199 to Met-205.			AR089: 1, AR061: 0			
573	HCMUSD61	927475	583	66 - 959	1483	Arg-17 to Asn-23, Arg-90 to Gly-95, Leu-114 to Glu-121, Pro-153 to Asp-158, Thr-288 to Lys-295.			AR061: 6, AR089: 5 L0775: 5, H0486: 3, H0648: 3, L0748: 3, L0758: 3, H0657: 2, S0358: 2, H0370: 2,			

574	HCEEC58	933866	584	1 - 327	1484				H0331: 2, H0040: 2, H0616: 2, S0152: 2, L0754: 2, L0747: 2, L0759: 2, S0192: 2, H0170: 1, H0664: 1, S0356: 1, S0222: 1, H0575: 1, H0196: 1, H0014: 1, H0373: 1, H0039: 1, H0622: 1, T0023: 1, L0483: 1, H0644: 1, L0142: 1, H0674: 1, H0090: 1, H0059: 1, S0422: 1, L0772: 1, L0768: 1, L0766: 1, L0774: 1, L0655: 1, H0547: 1, H0435: 1, H0659: 1, H0521: 1, S0027: 1, L0740: 1, L0756: 1, H0445: 1, L0593: 1, H0668: 1, L0462: 1 and H0352: 1.		
575	HSYAD06	935334	585	1 - 765	1485				AR089: 110, AR061: 37 S0007: 3, S0354: 2, H0529: 2, H0645: 1, H0052: 1 and H0039: 1. AR061: 4, AR089: 3		
576	HUSID53	943374	586	2 - 994	1486	Arg-1 to Glu-6,			AR089: 1, AR061: 1		

577	HRGDE77	948737	587	2 - 1051	1487	Lys-25 to Arg-32, Gly-53 to Asn-61, Asn-116 to Glu-121, Thr-194 to Thr-199, Asn-209 to Thr-217. Arg-20 to Leu-28, Phe-57 to Arg-79.	H0522: 2, H0052: 1, H0412: 1, L0794: 1, L0803: 1, H0651: 1, H0521: 1, L0748: 1, L0749: 1 and L0752: 1. AR089: 12, AR061: 8 L0751: 10, L0748: 9, S0222: 6, L0438: 4, L0747: 4, S0356: 3, H0040: 3, S0344: 3, L0766: 3, L0809: 3, L0665: 3, S0380: 3, L0758: 3, H0624: 2, S0360: 2, S0010: 2, H0014: 2, H0399: 2, H0622: 2, S0038: 2, S0144: 2, S0002: 2, L0770: 2, L0803: 2, H0666: 2, L0439: 2, L0749: 2, L0596: 2, L0595: 2, S0218: 1, S0400: 1, H0483: 1, S0045: 1, H0619: 1, H0393: 1, S0278: 1, H0250: 1, H0618: 1, H0253: 1, H0052: 1, H0457: 1, H0123: 1, H0242: 1, H0266: 1, H0687: 1, H0264: 1, H0102: 1, H0641: 1,		
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							H0646: 1, L0763: 1, L0771: 1, L0794: 1, L0804: 1, L0776: 1, L0807: 1, L0788: 1, L0664: 1, S0052: 1, H0144: 1, H0547: 1, H0689: 1, H0659: 1, H0648: 1, H0521: 1, H0696: 1, H0134: 1, L0779: 1 and L0605: 1.			
578	HEGAU68	950009	588	239 - 520	1488		AR089: 11, AR061: 4 L0744: 9, L0731: 8, L0439: 7, H0144: 5, L0749: 5, L0748: 4, L0745: 4, L0758: 4, S0040: 3, H0013: 3, H0038: 3, L0769: 3, L0773: 3, L0755: 3, H0306: 2, S0356: 2, S0358: 2, H0550: 2, H0392: 2, S0280: 2, H0620: 2, T0003: 2, H0598: 2, S0036: 2, H0623: 2, S0344: 2, S0002: 2, L0662: 2, L0768: 2, L0561: 2, L0775: 2, L0776: 2, L0527: 2, L0783: 2, L0438: 2, S0126: 2, H0539: 2, S0152: 2.			

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579	HNGKH38	951032	589	3 - 251	1489	AR061: 11, AR089: 5	H0135: 1, H0163: 1, H0634: 1, H0087: 1, H0412: 1, H0056: 1, S0038: 1, H0100: 1, T0041: 1, H0429: 1, S0450: 1, S0142: 1, S0426: 1, H0529: 1, L0763: 1, L0770: 1, L0796: 1, L0761: 1, L0667: 1, L0646: 1, L0764: 1, L0771: 1, L0766: 1, L0375: 1, L0655: 1, L0657: 1, L0659: 1, L0517: 1, L0383: 1, L0382: 1, L0543: 1, L0666: 1, L0664: 1, S0374: 1, H0520: 1, H0519: 1, H0689: 1, H0682: 1, H0659: 1, H0658: 1, S0328: 1, S0027: 1, L0740: 1, L0746: 1, L0750: 1, L0759: 1, H0445: 1, L0480: 1, L0584: 1, S0242: 1, S0276: 1, H0543: 1, H0423: 1, H0422: 1, S0446: 1, L0600: 1 and H0352: 1.
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580	HNHN26	952398	590	404 - 135	1490			H0069: 1, H0399: 1, S0428: 1, H0698: 1 and H0521: 1.			
581	HTEHP64	953791	591	304 - 2	1491	Asp-49 to Phe-54, Thr-89 to Ala-94.		AR089: 1, AR061: 0 S0216: 1 and S0390: 1. AR089: 625, AR061: 610 L0666: 6, S6028: 3, L0662: 3, L0663: 3, H0038: 2, L0768: 2, S0360: 1, S0045: 1, H0574: 1, S0010: 1, H0428: 1, H0169: 1, S0036: 1, H0616: 1, L0520: 1, L0796: 1, L0657: 1, L0792: 1, L0665: 1, S0053: 1, H0547: 1, H0684: 1, S0260: 1, H0445: 1, L0599: 1 and L0593: 1.	20q13.1	256540, 600281, 600281	
582	HMLAO78	953793	592	265 - 576	1492	Ser-5 to Ser-12.		AR089: 11, AR061: 4 L0666: 6, S6028: 3, L0662: 3, L0663: 3, H0038: 2, L0768: 2, S0360: 1, S0045: 1, H0574: 1, S0010: 1, H0428: 1, H0169: 1, S0036: 1, H0616: 1, L0520: 1, L0796: 1, L0657: 1, L0792: 1,	20q13.1	256540, 600281, 600281	

583	HFPCN94	955009	593	3 - 860	1493	Pro-3 to Gly-10.	L0665: 1, S0053: 1, H0547: 1, H0684: 1, S0260: 1, H0445: 1, L0599: 1 and L0593: 1. AR089: 5, AR061: 4 L0731: 6, H0539: 5, L0065: 4, L0775: 4, L0803: 3, L0776: 3, L0663: 3, L0755: 3, S0356: 2, H0632: 2, H0545: 2, H0551: 2, L0769: 2, L0764: 2, L0662: 2, L0794: 2, L0783: 2, L0666: 2, L0750: 2, L0759: 2, H0624: 1, H0170: 1, H0583: 1, L0005: 1, H0580: 1, H0550: 1, S0222: 1, H0370: 1, H0586: 1, H0098: 1, H0318: 1, H0510: 1, H0622: 1, H0032: 1, H0169: 1, H0212: 1, S0036: 1, H0634: 1, H0022: 1, H0494: 1, S0422: 1, L0520: 1, L0796: 1, L0761: 1, L0373: 1, L0372: 1, L0806: 1, L0659: 1, L0809: 1, H0660: 1,			
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								S0328: 1, S0380: 1, S0152: 1, H0696: 1, L0439: 1, L0754: 1, L0756: 1, L0777: 1, L0758: 1, H0445: 1, L0605: 1 and L0599: 1.			
584	HSLHV08	958582	594	167 - 3	1494			AR089: 1, AR061: 0 S0428: 1 and S0028: 1.			
585	HPDVW40	961039	595	3 - 629	1495	Thr-85 to Gly-92, Pro-159 to Asn-180.		AR089: 13, AR061: 7 L0804: 5, L0758: 5, L0740: 3, L0754: 3, L0777: 3, L0604: 3, L0770: 2, L0794: 2, H0658: 2, L0752: 2, L0759: 2, L0622: 1, T0060: 1, L0021: 1, T0001: 1, L0163: 1, H0553: 1, L0769: 1, L0662: 1, L0659: 1, L0529: 1, L0789: 1, L0792: 1, S0330: 1, L0747: 1, L0749: 1 and L0485: 1.			
586	HEMF70	961963	596	1 - 1164	1496	Leu-28 to Asp-35, Leu-59 to Ser-65, Glu-111 to Lys-117, Gln-131 to Ala-137, Asp-224 to Asp-233, Ala-262 to Trp-268.		AR089: 8, AR061: 5 S0046: 2, S0116: 1, S0356: 1, H0194: 1, H0051: 1, H0591: 1, H0634: 1, H0551: 1, L0564: 1, S0150: 1, H0538: 1, S0152: 1,			

							H0521: 1, S0206: 1 and H0543: 1.			
587	HLD0020	910371	597	2 - 157	1497	Pro-21 to Arg-28.	AR061: 5, AR089: 4 L0748: 2, L0749: 2, H0510: 1 and H0144: 1.			
		963284	886	24 - 1298	1786	Glu-29 to Gly-35,				
		963655	887	1 - 1281	1787	Leu-51 to Glu-59, Gly-91 to His-98.				
588	HSLEP67	963505	598	44 - 352	1498		AR061: 0, AR089: 0 S0428: 1, S0390: 1 and S0028: 1.			
589	HSLEP94	964463	599	429 - 1355	1499		AR061: 2, AR089: 1 S0028: 5, H0624: 2, S0031: 2, H0171: 1, S0282: 1, H0250: 1, H0617: 1, H0124: 1, H0059: 1, H0144: 1, S0146: 1 and S0260: 1.			
590	HSENS89	964527	600	1 - 891	1500	Leu-1 to Phe-16.	AR089: 5, AR061: 3 H0556: 2, S0218: 1, S0132: 1, H0553: 1, H0494: 1, S0126: 1, L0602: 1, S0027: 1, L0748: 1, H0667: 1, S0276: 1 and H0423: 1.			
591	HNTAF77	966190	601	509 - 3	1501		AR089: 1, AR061: 1 L0771: 3, S0222: 2, L0731: 2, H0295: 1, H0606: 1, L0770: 1,			

									L0783: 1, L0791: 1, H0519: 1, L0751: 1, L0779: 1, L0755: 1 and L0759: 1.			
592	HBIOV48	967566	602	25 - 537	1502	Ser-6 to Trp-15, Lys-18 to Gln-27, Pro-29 to Gly-35.			AR089: 0, AR061: 0 L0771: 4, L0803: 4, L0742: 4, L0770: 3, L0759: 3, H0194: 2, L0805: 2, L0776: 2, L0809: 2, L0789: 2, S0126: 2, S0328: 2, L0748: 2, L0779: 2, H0556: 1, S0354: 1, H0261: 1, S0010: 1, S0049: 1, H0052: 1, L0738: 1, H0105: 1, S0036: 1, H0135: 1, H0551: 1, H0538: 1, L0769: 1, L0761: 1, L0766: 1, L0649: 1, L0804: 1, L0774: 1, L0775: 1, L0659: 1, L0782: 1, L0787: 1, L0665: 1, H0593: 1, H0660: 1, H0672: 1, S0380: 1, L0741: 1, L0749: 1 and H0423: 1.			
593	HBGMN45	967744	603	2 - 562	1503				AR089: 1, AR061: 1 H0617: 2, S6028: 1 and S0028: 1.			

594	HBXCE20	970889	604	2 - 403	1504		AR089: 1, AR061: 0 S0031: 4, H0624: 2, S0050: 2, H0246: 1, S0038: 1 and S0260: 1.		
595	HSLJU88	780811	605	214 - 540	1505	Ser-29 to Gly-35, Thr-82 to Val-95.	AR061: 1, AR089: 1 S0390: 2, S0278: 1 and S0144: 1.		
596	HKGDQ60	863330	606	768 - 223	1506	Arg-1 to His-9, Pro-14 to Thr-20.	AR089: 5, AR061: 2 H0261: 3, H0046: 3, L0485: 2, H0052: 1, H0538: 1 and L0745: 1.		
597	HSDKF67	933059	607	2 - 469	1507	Asn-2 to Asp-7.	AR061: 4, AR089: 1 H0271: 1 and S0260: 1.		
598	HSLFT94	603023	608	3 - 323	1508	Lys-16 to Arg-23, Gln-55 to Ile-62, Pro-99 to Asn-105.	AR089: 1, AR061: 1 S0028: 2 and S0044: 1.		
599	HTJMD06	837603	609	2 - 424	1509	Lys-35 to Lys-41, Asp-82 to Arg-88, Thr-123 to Thr-128.	AR089: 2, AR061: 1 S6028: 1, H0488: 1 and H0056: 1.		
600	HNTBH68	851274	610	1 - 540	1510	Ala-51 to Ser-57, Glu-108 to Trp-113, Phe-138 to Glu-146.	AR089: 6, AR061: 3 L0005: 1, H0144: 1, L0438: 1, H0519: 1, H0539: 1 and L0439: 1.		
601	HMEKO39	863507	611	2 - 610	1511	Pro-67 to Pro-72.	AR061: 5, AR089: 3 L0741: 5, L0751: 4, L0777: 4, S0007: 3, H0575: 3, L0747: 3, L0592: 3, S0212: 2, H0545: 2, H0266: 2, L0769: 2, L0771: 2.		

									L0768: 2, L0794: 2, L0789: 2, H0144: 2, L0352: 2, S0028: 2, L0742: 2, L0439: 2, L0754: 2, L0779: 2, L0755: 2, S0418: 1, S0420: 1, S0376: 1, S0300: 1, H0438: 1, H0327: 1, H0009: 1, H0123: 1, H0594: 1, H0179: 1, H0271: 1, H0615: 1, H0628: 1, H0551: 1, S0038: 1, H0100: 1, S0464: 1, S0210: 1, L0369: 1, L0761: 1, L0800: 1, L0764: 1, L0521: 1, L0806: 1, L0659: 1, L0809: 1, L0367: 1, H0435: 1, S0152: 1, H0696: 1, L0756: 1, L0757: 1 and L0758: 1.					
602	HAABH11	965473	612	1 - 699	1512				AR089: 16, AR061: 5 L0740: 5, H0356: 2, H0413: 2, L0770: 2, L0777: 2, S0376: 1, S0360: 1, H0646: 1, L0763: 1 and L0747: 1.					
603	HUVFZ43	910860	613	3 - 1376	1513	Lys-68 to Lys-75, Lys-111 to Asn-120.			AR089: 13, AR061: 4 H0619: 2, H0056: 2,					

						Ser-137 to Leu-153, Gln-155 to Gly-162, Glu-169 to Gln-178, Ser-208 to Thr-213, Arg-239 to Gly-247, Lys-253 to Leu-259, Glu-275 to Glu-281.		S0132: 1, H0266: 1, H0623: 1, H0494: 1, L0769: 1 and S0152: 1.		
604	HCEPH84	910864	614	1689 - 706	1514	Ser-65 to Gly-75, Thr-84 to Ser-89.		AR089: 1, AR061: 1 L0439: 6, L0745: 5, H0052: 4, L0438: 4, L0592: 3, L0604: 3, H0009: 2, S0001: 1, H0599: 1, H0196: 1, H0172: 1, T0010: 1, S0364: 1, S0366: 1, S0038: 1, L0789: 1, H0144: 1, S0044: 1, L0747: 1, L0759: 1 and L0605: 1.		
605	HNFD052	916260	615	2 - 358	1515			AR089: 5, AR061: 5 H0083: 17, H0556: 14, H0265: 7, L0794: 6, H0271: 5, H0543: 5, L0766: 4, L0809: 4, H0635: 2, H0150: 2, S0114: 1, H0650: 1, H0645: 1, S0222: 1, H0438: 1, H0196: 1, H0594: 1, H0416: 1, H0615: 1, H0033: 1,	2q11	129490, 600334

606	HHEJR23	919082	616	864 - 205	1516	Lys-47 to Ile-60, Ser-102 to Lys-107, Lys-152 to Ser-158, Lys-171 to Glu-176.	H0087: 1, H0488: 1, S0142: 1, L0764: 1, L0803: 1, L0655: 1, L0657: 1, L0656: 1, L0659: 1, L0783: 1, L0790: 1, L0663: 1, L0665: 1, S0216: 1, H0670: 1, H0436: 1, L0758: 1, H0595: 1, H0542: 1 and H0422: 1.	Xp11.22- p11.21	300008, 300008, 300008, 300008, 300047, 301000, 301000, 301300, 301830, 305400, 308300, 309470, 309500, 309610, 311050
							AR089: 1, AR061: 0 L0758: 5, S0360: 3, L0768: 3, S0380: 3, L0731: 3, H0038: 2, S0372: 2, L0761: 2, L0766: 2, H0539: 2, L0755: 2, H0341: 1, S0110: 1, S0418: 1, H0637: 1, S0278: 1, S0222: 1, H0052: 1, L0040: 1, H0252: 1, H0169: 1, H0616: 1, H0560: 1, S0382: 1, L0763: 1, L0770: 1, L0769: 1, L0646: 1, L0764: 1, L0803: 1, L0804: 1, L0775: 1, L0518: 1, L0809: 1, L0529: 1, L0791: 1, L0664: 1, H0659: 1,		

									H0648: 1, S0406: 1, L0751: 1, L0754: 1, L0779: 1, L0757: 1, L0597: 1, H0667: 1, S0242: 1, H0542: 1, H0543: 1 and L0698: 1.			
607	HMTAX31	971343	617	1091 - 522	1517			Lys-24 to Lys-36, Asp-63 to Thr-70, Arg-139 to Lys-146, Leu-156 to Ala-171.	AR050: 40, AR051: 39, AR054: 37, AR089: 5, AR061: 1 L0777: 4, S0358: 2, S0126: 2, H0522: 2, S0116: 1, H0638: 1, H0443: 1, H0014: 1, H0379: 1, S0016: 1, S0374: 1, H0518: 1, H0521: 1 and L0740: 1.			
608	HKIY174	729217	618	3 - 347	1518			Tyr-14 to Ser-22.	AR061: 5, AR089: 3 S0045: 1, H0441: 1, H0590: 1 and L0741: 1.			
609	HSKEI21	760792	619	398 - 3	1519			Tyr-12 to Gly-19, Ser-90 to Pro-98.	AR061: 171, AR089: 34 L0751: 12, H0556: 9, L0596: 9, L0372: 5, H0265: 4, L0803: 4, S0404: 4, L0748: 4, L0758: 4, H0135: 3, L0665: 3, H0521: 3, L0742: 3, H0656: 2, H0341: 2, H0255: 2, S0418: 2, S0376: 2,			

	H0370: 2, H0575: 2, H0618: 2, H0253: 2, H0553: 2, H0038: 2, L0770: 2, L0646: 2, L0533: 2, L0375: 2, L0518: 2, L0666: 2, L0664: 2, S0238: 2, S0027: 2, L0439: 2, L0755: 2, L0759: 2, L0581: 2, H0395: 1, H0583: 1, H0484: 1, H0483: 1, H0662: 1, S0045: 1, S0046: 1, S0132: 1, H0550: 1, H0392: 1, H0586: 1, H0013: 1, H0250: 1, S0280: 1, H0599: 1, S0010: 1, H0052: 1, H0545: 1, H0046: 1, H0050: 1, H0083: 1, S6028: 1, H0687: 1, H0288: 1, S0022: 1, H0424: 1, H0111: 1, H0617: 1, H0606: 1, H0040: 1, H0616: 1, H0551: 1, H0269: 1, H0100: 1, T0042: 1, H0494: 1, H0132: 1, S0210: 1, L0762: 1, L0763: 1, L0769: 1, L0772: 1, L0374: 1,
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610	HKAFK68	869127	620	605 - 18	1520	L0645: 1, L0662: 1, L0626: 1, L0768: 1, L0794: 1, L0766: 1, L0388: 1, L0774: 1, L0806: 1, L0776: 1, L0659: 1, H0547: 1, H0519: 1, H0435: 1, H0672: 1, H0651: 1, S0330: 1, H0539: 1, H0518: 1, S0350: 1, H0134: 1, S3012: 1, S0037: 1, S3014: 1, S0028: 1, L0743: 1, L0744: 1, L0747: 1, L0750: 1, L0777: 1, L0780: 1, L0731: 1, L0587: 1, H0668: 1, S0196: 1, H0542: 1, H0422: 1, S0460: 1 and H0506: 1.		
						AR089: 3, AR061: 3 L0751: 12, H0556: 9, L0596: 8, L0372: 5, H0265: 4, L0803: 4, S0404: 4, L0748: 4, L0758: 4, H0135: 3, L0665: 3, H0521: 3, L0742: 3, H0656: 2, H0341: 2, H0255: 2, S0418: 2, S0376: 2,		

	H0370: 2, H0575: 2, H0618: 2, H0253: 2, H0553: 2, H0038: 2, L0770: 2, L0646: 2, L0533: 2, L0375: 2, L0518: 2, L0666: 2, L0664: 2, S0238: 2, S0027: 2, L0439: 2, L0755: 2, L0759: 2, L0581: 2, H0395: 1, H0583: 1, H0484: 1, H0483: 1, H0662: 1, S0045: 1, S0046: 1, S0132: 1, H0550: 1, H0392: 1, H0586: 1, H0013: 1, H0250: 1, S0280: 1, H0599: 1, S0010: 1, H0052: 1, H0545: 1, H0046: 1, H0050: 1, H0083: 1, S6028: 1, H0687: 1, H0288: 1, S0022: 1, H0424: 1, H0111: 1, H0617: 1, H0606: 1, H0040: 1, H0616: 1, H0551: 1, H0269: 1, H0100: 1, T0042: 1, H0494: 1, H0132: 1, S0210: 1, L0762: 1, L0763: 1, L0769: 1, L0772: 1, L0374: 1,	
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611	HSRBB92	905110	621	2 - 2011	1521	Leu-11 to Asn-16, Gly-164 to Glu-171, Leu-181 to Ser-186, Asp-193 to Ser-201, Glu-222 to Leu-229, Gln-238 to Tyr-245, Leu-256 to Asp-267, Gly-286 to Gln-301, Ser-311 to Ala-319, Glu-345 to Gly-351,	L0645: 1, L0662: 1, L0626: 1, L0768: 1, L0794: 1, L0766: 1, L0388: 1, L0774: 1, L0806: 1, L0776: 1, L0659: 1, H0547: 1, H0519: 1, H0435: 1, H0672: 1, H0651: 1, S0330: 1, H0539: 1, H0518: 1, S0350: 1, H0134: 1, S3012: 1, S0037: 1, S3014: 1, S0028: 1, L0743: 1, L0744: 1, L0747: 1, L0750: 1, L0777: 1, L0780: 1, L0731: 1, L0587: 1, H0668: 1, S0196: 1, H0542: 1, H0422: 1, S0460: 1 and H0506: 1.	AR089: 23, AR061: 4 L0779: 10, L0747: 8, L0758: 7, L0766: 4, L0776: 4, L0748: 4, L0740: 4, S0360: 3, H0616: 3, L0754: 3, L0731: 3, L0759: 3, L0599: 3, L0362: 3, H0543: 3, H0341: 2, H0013: 2, H0024: 2,	120260, 138140, 178300, 246450
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612	HWLLR80	931564	622	1 - 630	1522	Pro-14 to Thr-20,	Phe-361 to Asp-367, Thr-436 to Arg-443, Ile-460 to Gln-467, Gln-510 to Glu-533, Ala-541 to Ala-548, Gln-561 to Glu-571, Leu-581 to Ala-590, Phe-639 to Ser-652.	H0617: 2, L0769: 2, L0771: 2, L0662: 2, L0649: 2, L0806: 2, L0438: 2, S0328: 2, H0694: 2, L0439: 2, L0751: 2, L0780: 2, L0592: 2, L0608: 2, H0650: 1, L0785: 1, H0638: 1, H0208: 1, S0132: 1, H0370: 1, H0438: 1, H0592: 1, H0599: 1, H0421: 1, H0596: 1, T0110: 1, H0597: 1, L0163: 1, L0455: 1, L0456: 1, H0124: 1, S0366: 1, H0040: 1, H0551: 1, H0059: 1, S0386: 1, T0042: 1, H0334: 1, S0144: 1, L0763: 1, L0770: 1, L0761: 1, L0772: 1, L0764: 1, L0774: 1, L0659: 1, L0789: 1, H0144: 1, H0520: 1, H0547: 1, H0658: 1, H0670: 1, S0378: 1, H0521: 1, L0749: 1, S0011: 1 and H0653: 1.	AR089: 2, AR061: 2	
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613	HWLWQ87	932577	623	76 - 519	1523	Glu-44 to Gly-50, Pro-104 to Gly-111, Gly-127 to Leu-132, Asn-146 to Asp-151, Asn-165 to Glu-170, Ser-194 to Asp-202. Ile-11 to Glu-19.	S0358: 1, H0370: 1, H0253: 1, H0040: 1, H0547: 1, L0601: 1 and S0196: 1. AR089: 23, AR061: 12 L0731: 6, L0766: 5, L0759: 5, L0471: 2, H0038: 2, L0748: 2, L0740: 2, L0758: 2, L0590: 2, S0360: 1, H0596: 1, H0046: 1, L0483: 1, H0644: 1, H0616: 1, H0509: 1, H0647: 1, S0210: 1, L0648: 1, L0363: 1, L0774: 1, L0775: 1, L0657: 1, L0526: 1, L0666: 1, L0664: 1, S0126: 1, H0672: 1, L0744: 1, L0593: 1, L0595: 1, H0665: 1 and S0194: 1.		
614	H6EEP53	942872	624	3 - 1595	1524		AR061: 1, AR089: 1 L0748: 8, L0769: 7, L0758: 7, L0749: 5, H0135: 4, S0418: 3, S0358: 3, H0618: 3, H0424: 3, H0529: 3.		

	L0439: 3, L0747: 3, L0779: 3, L0777: 3, H0265: 2, S0356: 2, S0360: 2, S0278: 2, H0257: 2, H0559: 2, H0156: 2, H0596: 2, H0232: 2, H0544: 2, H0510: 2, H0031: 2, H0087: 2, T0041: 2, H0494: 2, S0344: 2, L0764: 2, L0766: 2, L0664: 2, L0438: 2, H0547: 2, H0539: 2, H0522: 2, H0555: 2, L0751: 2, L0757: 2, L0587: 2, L0605: 2, L0411: 1, H0686: 1, H0295: 1, H0341: 1, S0001: 1, H0483: 1, H0255: 1, H0664: 1, H0306: 1, H0458: 1, S0376: 1, H0580: 1, L0717: 1, H0550: 1, S0222: 1, H0592: 1, H0497: 1, L0622: 1, H0013: 1, H0253: 1, H0318: 1, H0052: 1, H0546: 1, H0046: 1, H0012: 1, H0373: 1, H0083: 1, H0399: 1, H0288: 1, H0290: 1,						
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615	HE2KZ56	968439	625	82 - 342	1525	H0252: 1, T0006: 1, H0213: 1, H0553: 1, H0644: 1, H0673: 1, H0068: 1, H0038: 1, H0040: 1, H0551: 1, H0413: 1, H0100: 1, H0131: 1, S0150: 1, S0144: 1, S0422: 1, L0369: 1, L0763: 1, L0646: 1, L0643: 1, L0645: 1, L0773: 1, L0662: 1, L0768: 1, L0364: 1, L0650: 1, L0774: 1, L0775: 1, L0378: 1, L0776: 1, L0657: 1, L0659: 1, L0783: 1, L0666: 1, L0665: 1, S0428: 1, H0144: 1, H0520: 1, H0519: 1, H0435: 1, H0658: 1, H0666: 1, H0518: 1, H0521: 1, H0696: 1, L0609: 1, S3014: 1, S0027: 1, L0741: 1, L0744: 1, L0754: 1, L0752: 1, L0731: 1, L0759: 1, L0596: 1, H0665: 1, H0423: 1 and S0446: 1.	AR089: 2, AR061: 1
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616	HFXHD52	490721	626	191 - 3	1526	Asn-44 to Ala-51.	H0624: 2 and S0031: 1. S0001: 1, S0045: 1 and S0216: 1.		
		883683	888	1 - 279	1788	Phe-2 to Ser-8, Glu-58 to Gln-63, Asn-74 to Leu-81.			
617	HPMAM67	915879	627	2 - 64	1527		L0777: 20, L0439: 11, L0747: 10, S0360: 6, L0766: 6, L0758: 6, L0717: 5, H0521: 5, H0038: 3, S0330: 3, L0752: 3, L0755: 3, L0599: 3, S0358: 2, H0581: 2, S0003: 2, S0214: 2, H0068: 2, L0764: 2, L0662: 2, L0655: 2, L0666: 2, L0665: 2, H0648: 2, L0740: 2, L0751: 2, L0749: 2, L0750: 2, L0731: 2, L0757: 2, S0031: 2, L0596: 2, L0581: 2, L0362: 2, S0192: 2, H0542: 2, S0040: 1, H0650: 1, H0657: 1, S0282: 1, H0580: 1, H0393: 1, H0586: 1, H0574: 1, H0486: 1, L0586: 1, H0013: 1, L0021: 1,		

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619	HELGM94						Lys-57 to Pro-62, Ser-108 to Ala-114, Asp-133 to Arg-140, Arg-173 to Asn-183.	L0608: 3, H0624: 1, H0589: 1, H0438: 1, H0250: 1, S0050: 1, H0135: 1, S0144: 1, H0689: 1 and S0028: 1.		
		566768	890	489 - 1295	1790		Cys-32 to Cys-39, Glu-47 to Pro-52, Lys-57 to Pro-62, Ser-108 to Ala-114, Asp-133 to Arg-140, Arg-173 to Asn-183.			
		847653	891	30 - 647	1791		Asp-72 to Glu-78, Ser-103 to Glu-110, Lys-112 to His-117.			
		847655	892	748 - 1923	1792		Lys-42 to Pro-47, Ser-93 to Ala-99, Asp-118 to Arg-125, Arg-158 to Asn-168, Ala-251 to Val-263, His-287 to Tyr-292, Glu-302 to Gln-307.			
		913938	629	1 - 1437	1529		Gly-1 to Ser-8, Arg-10 to Ser-15, Leu-17 to Gly-22, Lys-115 to Ala-130, Tyr-149 to Gly-156, Asn-181 to Glu-190, Glu-252 to Glu-257, Ser-339 to Asp-347, Leu-356 to Leu-361,	AR089: 9, AR061: 5, H0584: 5, H0599: 5, H0556: 4, H0124: 4, H0559: 3, H0622: 3, H0341: 2, H0125: 2, S0045: 2, H0620: 2, H0024: 2, T0042: 2, L0665: 2, H0144: 2, H0265: 1, S6024: 1,	16p11.2	147781, 172471, 182381

						Ser-387 to Lys-395, Thr-470 to Ile-476.	H0583: 1, H0208: 1, S0046: 1, H0393: 1, S0278: 1, H0549: 1, H0550: 1, H0438: 1, H0586: 1, H0486: 1, H0250: 1, S0280: 1, H0618: 1, H0253: 1, H0009: 1, H0687: 1, H0284: 1, H0424: 1, H0031: 1, S0366: 1, H0116: 1, H0056: 1, S0038: 1, H0494: 1, H0132: 1, H0131: 1, H0130: 1, L0662: 1, L0803: 1, S0428: 1, S0216: 1, S0126: 1, H0518: 1, S0152: 1, S0118: 1, S3014: 1, L0759: 1 and S0011: 1.		
620	HLJDQ52	923110	630	3 - 824	1530	Gly-26 to Val-70, Ser-199 to Arg-204.	AR089: 15, AR061: 1 T0109: 1, H0013: 1, H0375: 1, H0509: 1, H0519: 1, H0690: 1, S0152: 1 and L0485: 1.		
621	HAAJAW40	1219455	631	68 - 2323	1531	Pro-7 to Arg-12, Leu-32 to His-52, Tyr-54 to Asp-69, Pro-74 to Gly-92, Glu-99 to Arg-125, Asp-130 to Glu-142,	AR089: 4, AR061: 1 L0803: 5, L0731: 4, L0662: 3, L0665: 3, S0276: 3, H0486: 2, H0575: 2, H0318: 2, L0794: 2, L0805: 2,		

622	HATAZ67	825697 1106635	893 632	1 - 765 2 - 598	1793 1532	<p>Thr-144 to Ala-153, Arg-197 to Lys-202, Leu-214 to Pro-227, Asp-245 to Arg-251, Gly-261 to Gln-267, Gly-283 to His-288, Ser-326 to Gln-336, Met-356 to Glu-361, Ala-438 to Ile-444, Ser-479 to Val-484, Arg-490 to Arg-499, Pro-509 to Gln-514, Glu-622 to Ser-628, Thr-653 to Arg-658, Glu-678 to Asp-752.</p> <p>L0776: 2, L0809: 2, L0663: 2, H0684: 2, L0740: 2, L0759: 2, L0592: 2, H0624: 1, L0448: 1, H0341: 1, S0282: 1, H0663: 1, S0360: 1, H0580: 1, L0468: 1, H0587: 1, H0427: 1, S0010: 1, L0471: 1, H0644: 1, H0169: 1, L0456: 1, H0090: 1, H0264: 1, H0412: 1, H0561: 1, S0150: 1, S0002: 1, H0529: 1, L0638: 1, L0372: 1, L0649: 1, L0388: 1, L0659: 1, L0783: 1, L0789: 1, L0791: 1, H0519: 1, S0380: 1, H0522: 1, H0436: 1, L0747: 1, L0752: 1, L0757: 1, L0599: 1, H0542: 1, H0543: 1 and H0422: 1.</p>	
						<p>AR061: 0, AR089: 0 H0038: 3, H0156: 2, L0455: 1, H0616: 1, S0038: 1, H0538: 1 and S0028: 1</p>	

623	HBUAC02	908326	894	3 - 809	1794	Asn-23 to Trp-32, Ile-49 to Asp-56, Gln-85 to Pro-91. Ala-8 to Thr-23, Pro-35 to Met-41, Asn-60 to Thr-65, Asn-89 to Glu-94, Pro-161 to Leu-167, Asp-184 to Trp-189, Phe-192 to Leu-206, Arg-215 to Leu-221.	AR089: 13, AR061: 8 S0152: 4, H0556: 3, H0265: 2, S3014: 2, H0543: 2, H0423: 2, H0161: 1, H0650: 1, H0402: 1, S0045: 1, S0046: 1, H0393: 1, H0599: 1, H0575: 1, H0618: 1, H0253: 1, S0182: 1, H0083: 1, H0594: 1, H0247: 1, H0124: 1, H0652: 1, S0144: 1, H0519: 1, H0651: 1, S0027: 1 and H0445: 1.			
624	HCWEQ14	933546	895	3 - 818	1795	Ala-8 to Thr-23, Pro-35 to Met-41, Asn-60 to Thr-65, Asn-89 to Glu-94, Pro-161 to Leu-167, Asp-184 to Trp-189, Phe-192 to Pro-201, Pro-226 to Lys-231, Ala-237 to Pro-264.				
		1117318	634	319 - 77	1534		AR089: 39, AR061: 8 H0305: 3			
		908245	896	1 - 177	1796	Leu-43 to Tyr-48.				

625	HDPWH41	1228148	635	1 - 642	1535	AR089: 6, AR061: 2 S0252: 5, S0268: 5, S0256: 4, S0228: 3, S0270: 3, S0258: 2, H0305: 2, H0090: 2, H0521: 2, L0740: 2, L0777: 2, H0657: 1, S0212: 1, H0661: 1, H0580: 1, L0717: 1, H0438: 1, H0486: 1, T0074: 1, H0581: 1, S0388: 1, H0412: 1, L0637: 1, L0766: 1, L0791: 1, S0216: 1, H0670: 1, S0380: 1, L0755: 1, H0445: 1, L0605: 1, L0592: 1, L0581: 1, L0593: 1 and H0543: 1.		
626	HDQEH61	1213567	636	46 - 867	1536	AR089: 63, AR061: 13 H0616: 3, H0521: 3, H0046: 2, H0038: 2, S0045: 1, H0550: 1, H0013: 1, S0386: 1, H0494: 1, S0150: 1, H0520: 1, H0436: 1 and L0595: 1.		
		772569	897	1 - 369	1797	Arg-68 to Ser-76.		
		908303	898	2 - 766	1798	Gln-49 to Thr-58, Pro-175 to Lys-184.		

627	HDTDD72	587710	637	162 - 371	1537		AR089: 159, AR061: 142 H0486: 1	17p13.3	113721, 247200, 600059, 601545
628	HFRBN02	1152485	638	2 - 967	1538	Gly-114 to Gly-120, Pro-140 to Tyr-145, Asn-180 to Gly-185, Arg-274 to Ala-280, Gly-310 to Gly-317.	AR089: 3, AR061: 1 S0045: 1, S0050: 1, H0020: 1 and S0032: 1.		
		973667	899	2 - 409	1799	Gly-114 to Gly-120.			
		1107045	639	1 - 642	1539	Pro-9 to Ala-19, Ser-39 to Gly-46, Thr-54 to Gly-62, Ile-77 to Arg-84, Thr-122 to Met-132, Gln-134 to Gln-147.			
629	HKAJH72						AR089: 2, AR061: 2 L0766: 2, L0665: 2, H0395: 1, S0212: 1, S0360: 1, H0551: 1, H0494: 1, L0639: 1, L0521: 1, L0804: 1, H0682: 1 and L0749: 1.		
630	HMAAD90	761293	900	1 - 690	1800	Pro-9 to Ala-19, Ser-39 to Gly-46, Thr-54 to Gly-62, Ile-77 to Arg-84, Thr-122 to Met-132, Gln-134 to Gln-147.	AR089: 2, AR061: 1 L0769: 7, L0783: 6, L0775: 5, L0748: 4, L0758: 4, L0622: 3, H0599: 3, H0373: 3, L0772: 3, L0777: 3, L0757: 3, S0045: 2.		
		1152487	640	334 - 2	1540	Ser-15 to Gln-23, Gly-79 to Asp-92, Gly-105 to Cys-111.			

963983	901	1523 - 171	1801	Asp-26 to Arg-32, Arg-74 to Leu-79, Ser-83 to Cys-95, Leu-108 to Thr-118, Gly-126 to Gly-131, Arg-162 to Pro-168	L0021: 2, S0366: 2, S0144: 2, L0774: 2, L0541: 2, S0310: 2, L0604: 2, L0808: 1, S0116: 1, S0376: 1, S0360: 1, H0404: 1, L0468: 1, H0587: 1, L0623: 1, H0156: 1, T0048: 1, S0324: 1, S0049: 1, H0530: 1, N0006: 1, H0081: 1, H0428: 1, H0622: 1, H0213: 1, H0674: 1, H0087: 1, H0379: 1, L0520: 1, L0764: 1, L0521: 1, L0525: 1, L0663: 1, S0126: 1, H0684: 1, H0660: 1, H0576: 1, S0027: 1, L0747: 1, L0779: 1, L0752: 1, L0759: 1, S0031: 1, L0485: 1, H0423: 1, S0462: 1 and H0352: 1.
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631	HMABQ71	1105540	641	3 - 374	1541	His-173 to Asp-178, Arg-196 to Ser-202, Arg-214 to Val-220, Ser-243 to Leu-253, Arg-275 to Ile-283, Lys-367 to Phe-374, Gln-384 to Gly-389, Glu-430 to Lys-440.	AR089: 1, AR061: 0 S0144: 1 and H0521: 1.		
632	HPJEV95	729831	902	189 - 497	1802		AR061: 4, AR089: 1 S0152: 1 and L0601: 1.		
633	HSKYR59	929723	903	82 - 408	1803	His-91 to Gly-103, Gly-112 to Gly-117, Glu-129 to Glu-136, Gly-146 to Gly-151, Arg-168 to Glu-184, Arg-203 to Arg-210.	AR061: 16, AR089: 6 H0617: 10, S0358: 5, L0622: 4, H0620: 4, H0658: 4, L0623: 3, H0424: 3, H0549: 2, H0550: 2, H0586: 2, H0486: 2, H0546: 2, L0769: 2, L0773: 2, S0374: 2, S0206: 2, L0743: 2, L0750: 2, L0779: 2, L0731: 2, L0601: 2, H0624: 1, H0170: 1, H0171: 1, H0686: 1, H0295: 1, H0657: 1, H0484: 1, H0255: 1, S0420: 1,		
		1219545	643	154 - 783	1543				

634	HSWAM16	933750	904	1 - 360	1804	S0376: 1, S0360: 1, H0370: 1, H0455: 1, H0587: 1, T0060: 1, T0114: 1, H0599: 1, H0122: 1, H0327: 1, H0544: 1, H0545: 1, H0188: 1, H0688: 1, T0006: 1, H0213: 1, H0606: 1, H0673: 1, S0364: 1, S0366: 1, H0634: 1, H0087: 1, H0413: 1, H0334: 1, S0144: 1, L0598: 1, L0763: 1, L0796: 1, L0639: 1, L0761: 1, L0772: 1, L0373: 1, L0764: 1, L0774: 1, L0775: 1, L0783: 1, L0809: 1, L0666: 1, L0663: 1, H0651: 1, S0378: 1, H0521: 1, S0392: 1, H0478: 1, L0751: 1, L0747: 1, L0752: 1, L0755: 1, L0757: 1, H0445: 1, L0608: 1, L0361: 1, L0366: 1, H0542: 1 and H0543: 1.	AR089: 4, AR061: 3
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	H0617: 10, S0358: 5, L0622: 4, H0620: 4, H0658: 4, L0623: 3, H0424: 3, H0549: 2, H0550: 2, H0586: 2, H0486: 2, H0546: 2, L0769: 2, L0773: 2, S0374: 2, S0206: 2, L0743: 2, L0750: 2, L0779: 2, L0731: 2, L0601: 2, H0624: 1, H0170: 1, H0171: 1, H0686: 1, H0295: 1, H0657: 1, H0484: 1, H0255: 1, S0420: 1, S0376: 1, S0360: 1, H0370: 1, H0455: 1, H0587: 1, T0060: 1, T0114: 1, H0599: 1, H0122: 1, H0327: 1, H0544: 1, H0545: 1, H0188: 1, H0688: 1, T0006: 1, H0213: 1, H0606: 1, H0673: 1, S0364: 1, S0366: 1, H0634: 1, H0087: 1, H0413: 1, H0334: 1, S0144: 1, L0598: 1, L0763: 1, L0796: 1, L0639: 1, L0761: 1, L0772: 1, L0373: 1,
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635	HSXCW82	1164013	645	123 - 1442	1545	Ala-2 to Gly-15, Glu-120 to Ser-125.	L0764: 1, L0774: 1, L0775: 1, L0783: 1, L0809: 1, L0666: 1, L0663: 1, H0651: 1, S0378: 1, H0521: 1, S0392: 1, H0478: 1, L0751: 1, L0747: 1, L0752: 1, L0755: 1, L0757: 1, H0445: 1, L0608: 1, L0361: 1, L0366: 1, H0542: 1 and H0543: 1.		
		933749	905	11 - 604	1805	Leu-14 to Ile-19, Pro-69 to Pro-76, Glu-86 to Thr-91, Val-121 to Thr-127, Phe-183 to Gln-188, Gly-282 to Lys-291, Arg-337 to Asn-346.	AR061: 6, AR089: 5 H0556: 8, H0617: 6, L0659: 6, L0666: 6, L0596: 6, H0441: 5, L0665: 5, S0222: 4, T0010: 4, S0038: 4, H0657: 3, H0559: 3, H0013: 3, H0494: 3, L0804: 3, L0809: 3, H0547: 3, S0152: 3, H0521: 3, H0265: 2, H0656: 2, L0717: 2, S0278: 2, H0250: 2, H0575: 2, S0049: 2, H0620: 2, H0288: 2, H0213: 2, S0036: 2,		

	H0634: 2, H0623: 2, L0764: 2, L0766: 2, L0775: 2, L0438: 2, H0682: 2, S0028: 2, L0779: 2, L0758: 2, L0595: 2, H0422: 2, H0224: 1, S0430: 1, L0785: 1, H0341: 1, S0212: 1, H0663: 1, S0420: 1, H0637: 1, H0580: 1, H0437: 1, H0282: 1, H0249: 1, T0109: 1, H0244: 1, H0069: 1, S0346: 1, H0318: 1, H0052: 1, H0194: 1, N0006: 1, L0471: 1, H0024: 1, H0057: 1, L0163: 1, H0107: 1, H0083: 1, H0594: 1, S0336: 1, H0070: 1, T0006: 1, H0644: 1, H0181: 1, H0135: 1, H0090: 1, H0040: 1, H0087: 1, H0059: 1, H0100: 1, L0351: 1, T0041: 1, H0429: 1, H0647: 1, S0210: 1, S0002: 1, H0529: 1, L0369: 1, L0769: 1, L0761: 1, L0372: 1, L0800: 1,	
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636	HSYDB42	739372	906	115 - 387	1806	Leu-14 to Ile-19.	L0794: 1, L0803: 1, L0806: 1, L0509: 1, L0657: 1, L0383: 1, L0787: 1, L0663: 1, S0374: 1, H0593: 1, H0658: 1, H0522: 1, H0134: 1, H0555: 1, L0612: 1, S3012: 1, S0037: 1, S3014: 1, S0206: 1, L0439: 1, L0749: 1, L0752: 1, S0031: 1, L0592: 1, L0608: 1, L0366: 1, H0667: 1, S0276: 1, H0542: 1 and H0423: 1.
		933545	646	2 - 631	1546	Arg-1 to Thr-11, Pro-23 to Met-29, Asn-48 to Thr-53, Asn-77 to Glu-82, Pro-149 to Leu-155, Asp-172 to Trp-177, Phe-180 to Leu-194, Arg-203 to Leu-209.	AR061: 2, AR089: 1 H0305: 5, L0766: 3, L0748: 3, H0265: 2, H0556: 2, H0551: 2, H0494: 2, L0770: 2, L0758: 2, L0599: 2, L0361: 2, H0650: 1, H0657: 1, H0381: 1, H0419: 1, H0427: 1, H0618: 1, H0421: 1, H0530: 1, H0546: 1, H0413: 1, H0625: 1, L0369: 1, L0644: 1, L0521: 1, L0375: 1,
							22q13.1-q13.2
							103050, 103050, 124030, 124030, 138981, 182380, 188826, 190040, 190040, 190040

637	HTXKJ79	1193059	647	2 - 421	1547	Pro-3 to Leu-9, Glu-12 to Val-22, Gln-27 to Glu-33, Pro-68 to Glu-75.	AR089: 3, AR061: 3 L0748: 9, S0356: 8, S0358: 8, L0471: 5, H0144: 5, L0740: 5, H0543: 5, H0574: 4, H0556: 3, S0354: 3, S0360: 3, S0049: 3, H0083: 3, T0042: 3, H0494: 3, S0374: 3, H0134: 3, H0436: 3, H0624: 2, H0663: 2, S0007: 2, S0132: 2, H0486: 2, H0013: 2, H0036: 2, H0251: 2, H0009: 2, S0036: 2, H0412: 2, H0561: 2, S0142: 2, H0522: 2, L0750: 2, L0588: 2, H0159: 1, H0583: 1, H0656: 1, H0341: 1, S0212: 1, H0240: 1, H0125: 1, S0418: 1, S0420: 1, S0410: 1,	L0783: 1, L0809: 1, L0789: 1, H0144: 1, S0374: 1, L0565: 1, H0658: 1, S0330: 1, H0539: 1, L0777: 1, L0731: 1, H0542: 1 and H0506: 1.			
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						S0045: 1, H0411: 1, H0369: 1, H0586: 1, H0497: 1, H0643: 1, H0331: 1, S0010: 1, H0052: 1, H0327: 1, H0544: 1, H0545: 1, H0011: 1, H0012: 1, H0014: 1, H0015: 1, H0239: 1, H0266: 1, H0688: 1, H0124: 1, H0135: 1, H0040: 1, H0413: 1, H0059: 1, H0280: 1, S0344: 1, H0529: 1, H0691: 1, H0547: 1, H0519: 1, H0682: 1, H0660: 1, S0328: 1, H0518: 1, H0521: 1, S0037: 1, S3014: 1, S0028: 1, L0742: 1, L0752: 1, L0755: 1, S0026: 1, H0136: 1 and H0293: 1.		
638	HUSGQ19	938963 1165320	907 648	99 - 443 556 - 1251	1807 1548	Gly-1 to Val-6, Ser-31 to Asn-41, Ser-61 to Lys-66, Lys-99 to Asn-105, Glu-190 to Thr-197. AR089: 2, AR061: 2 S0252: 5, S0268: 5, S0256: 4, S0228: 3, S0270: 3, S0258: 2, H0305: 2, H0090: 2, H0521: 2, L0740: 2, L0777: 2, H0657: 1,		

							S0212: 1, H0661: 1, H0580: 1, L0717: 1, H0438: 1, H0486: 1, T0074: 1, H0581: 1, S0388: 1, H0412: 1, L0637: 1, L0766: 1, L0791: 1, S0216: 1, H0670: 1, S0380: 1, L0755: 1, H0445: 1, L0605: 1, L0592: 1, L0581: 1, L0593: 1 and H0543: 1.		
639	HUSZS75	1193982	908	2 - 517	1808	Arg-1 to Asp-13, Arg-81 to Ser-89, Gly-128 to Gly-143.			AR089: 1, AR061: 1 L0769: 10, L0754: 10, L0766: 5, L0803: 4, L0756: 4, L0779: 4, L0780: 4, L0748: 3, L0753: 3, H0620: 2, H0264: 2, L0770: 2, L0806: 2, L0741: 2, L0747: 2, L0604: 2, H0265: 1, H0556: 1, H0657: 1, H0656: 1, H0341: 1, H0392: 1, H0331: 1, H0559: 1, H0427: 1, L0021: 1, H0173: 1, H0052: 1,

640	HWBDR25	908443	909	64 - 918	1809	Arg-7 to Thr-13.	<p>TO115: 1, H0188: 1, H0135: 1, H0413: 1, H0561: 1, H0647: 1, L0763: 1, L0761: 1, L0373: 1, L0768: 1, L0774: 1, L0651: 1, L0776: 1, L0659: 1, L0809: 1, L0787: 1, L0791: 1, L0792: 1, H0684: 1, H0521: 1, L0777: 1, L0752: 1, L0759: 1 and L0485: 1.</p>		
		908443	909	64 - 918	1809	Arg-7 to Thr-13.			
		1174365	650	3 - 1259	1550	Pro-1 to Glu-13, Gln-29 to Asn-35, Tyr-38 to Asn-43, Ala-102 to Ser-108, Arg-124 to Ile-134, Asp-172 to Asp-180, Lys-247 to Asn-252, Gly-336 to Trp-342.	<p>AR089: 5, AR061: 1 H0551: 2, S0420: 1, H0580: 1, H0586: 1, S0002: 1, H0435: 1 and H0521: 1.</p>		
		659873	910	3 - 542	1810	Lys-37 to Asn-42, Gly-126 to Trp-132.			
641	HBGSS51	954855	651	341 - 3	1551		<p>AR061: 5, AR089: 4 L0771: 12, H0040: 2, H0539: 2, H0306: 1, H0617: 1 and H0135: 1.</p>		

[42] The first column in Table 1A provides the gene number in the application corresponding to the clone identifier. The second column in Table 1A provides a unique "Clone ID NO:Z" for a cDNA clone related to each contig sequence disclosed in Table 1A. This clone ID references the cDNA clone which contains at least the 5' most sequence of the assembled contig and at least a portion of SEQ ID NO:X was determined by directly sequencing the referenced clone. The reference clone may have more sequence than described in the sequence listing or the clone may have less. In the vast majority of cases, however, the clone is believed to encode a full-length polypeptide. In the case where a clone is not full-length, a full-length cDNA can be obtained by methods described elsewhere herein.

[43] The third column in Table 1A provides a unique "Contig ID" identification for each contig sequence. The fourth column provides the "SEQ ID NO:" identifier for each of the contig polynucleotide sequences disclosed in Table 1A. The fifth column, "ORF (From-To)", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence "SEQ ID NO:X" that delineate the preferred open reading frame (ORF) shown in the sequence listing and referenced in Table 1A, column 6, as SEQ ID NO:Y. Where the nucleotide position number "To" is lower than the nucleotide position number "From", the preferred ORF is the reverse complement of the referenced polynucleotide sequence.

[44] The sixth column in Table 1A provides the corresponding SEQ ID NO:Y for the polypeptide sequence encoded by the preferred ORF delineated in column 5. In one embodiment, the invention provides an amino acid sequence comprising, or alternatively consisting of, a polypeptide encoded by the portion of SEQ ID NO:X delineated by "ORF (From-To)". Also provided are polynucleotides encoding such amino acid sequences and the complementary strand thereto.

[45] Column 7 in Table 1A lists residues comprising epitopes contained in the polypeptides encoded by the preferred ORF (SEQ ID NO:Y), as predicted using the algorithm of Jameson and Wolf, (1988) Comp. Appl. Biosci. 4:181-186. The Jameson-Wolf antigenic analysis was performed using the computer program PROTEAN (Version 3.11 for the Power MacIntosh, DNASTAR, Inc., 1228 South Park Street Madison, WI). In specific embodiments, polypeptides of the invention comprise, or alternatively consist of, at least one, two, three, four, five or more of the predicted epitopes as described in Table 1A.

It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly.

[46] Column 8 in Table 1A provides an expression profile and library code: count for each of the contig sequences (SEQ ID NO:X) disclosed in Table 1A, which can routinely be combined with the information provided in Table 4 and used to determine the tissues, cells, and/or cell line libraries which predominantly express the polynucleotides of the invention. The first number in column 8 (preceding the colon), represents the tissue/cell source identifier code corresponding to the code and description provided in Table 4. For those identifier codes in which the first two letters are not "AR", the second number in column 8 (following the colon) represents the number of times a sequence corresponding to the reference polynucleotide sequence was identified in the tissue/cell source. Those tissue/cell source identifier codes in which the first two letters are "AR" designate information generated using DNA array technology. Utilizing this technology, cDNAs were amplified by PCR and then transferred, in duplicate, onto the array. Gene expression was assayed through hybridization of first strand cDNA probes to the DNA array. cDNA probes were generated from total RNA extracted from a variety of different tissues and cell lines. Probe synthesis was performed in the presence of ³³P dCTP, using oligo(dT) to prime reverse transcription. After hybridization, high stringency washing conditions were employed to remove non-specific hybrids from the array. The remaining signal, emanating from each gene target, was measured using a Phosphorimager. Gene expression was reported as Phosphor Stimulating Luminescence (PSL) which reflects the level of phosphor signal generated from the probe hybridized to each of the gene targets represented on the array. A local background signal subtraction was performed before the total signal generated from each array was used to normalize gene expression between the different hybridizations. The value presented after "[array code]:" represents the mean of the duplicate values, following background subtraction and probe normalization. One of skill in the art could routinely use this information to identify normal and/or diseased tissue(s) which show a predominant expression pattern of the corresponding polynucleotide of the invention or to identify polynucleotides which show predominant and/or specific tissue and/or cell expression.

[47] Column 9 in Table 1A provides a chromosomal map location for certain polynucleotides of the invention. Chromosomal location was determined by finding exact matches to EST and cDNA sequences contained in the NCBI (National Center for Biotechnology Information) UniGene database. Each sequence in the UniGene database is

assigned to a "cluster"; all of the ESTs, cDNAs, and STSs in a cluster are believed to be derived from a single gene. Chromosomal mapping data is often available for one or more sequence(s) in a UniGene cluster; this data (if consistent) is then applied to the cluster as a whole. Thus, it is possible to infer the chromosomal location of a new polynucleotide sequence by determining its identity with a mapped UniGene cluster.

[48] A modified version of the computer program BLASTN (Altschul et al., J. Mol. Biol. 215:403-410 (1990); and Gish and States, Nat. Genet. 3:266-272 (1993)) was used to search the UniGene database for EST or cDNA sequences that contain exact or near-exact matches to a polynucleotide sequence of the invention (the 'Query'). A sequence from the UniGene database (the 'Subject') was said to be an exact match if it contained a segment of 50 nucleotides in length such that 48 of those nucleotides were in the same order as found in the Query sequence. If all of the matches that met this criteria were in the same UniGene cluster, and mapping data was available for this cluster, it is indicated in Table 1A under the heading "Cytologic Band". Where a cluster had been further localized to a distinct cytologic band, that band is disclosed; where no banding information was available, but the gene had been localized to a single chromosome, the chromosome is disclosed.

[49] Once a presumptive chromosomal location was determined for a polynucleotide of the invention, an associated disease locus was identified by comparison with a database of diseases which have been experimentally associated with genetic loci. The database used was the Morbid Map, derived from OMIM™ (*supra*). If the putative chromosomal location of a polynucleotide of the invention (Query sequence) was associated with a disease in the Morbid Map database, an OMIM reference identification number was noted in column 10, Table 1A, labelled "OMIM Disease Reference(s)". Table 5 is a key to the OMIM reference identification numbers (column 1), and provides a description of the associated disease in Column 2.

TABLE 1B

Clone ID NO:Z	SEQ ID NO:X	CONTIG ID:	BAC ID: A	SEQ ID NO:B	EXON From-To
HADTU18	26	666268	AC067849	1811	1-1270
HADTU18	26	666268	AC067849	1812	1-408
HYAAH23	42	1032585	AL158156	1813	1-134 381-1154 1539-2051 2660-4011 4082-4116 4578-5063 5736-6373 6388-6981 7052-7364 7527-7659 7698-7943 9535-9659 9671-10133 11759-12221
HYAAH23	42	1032585	AL158155	1814	1-171 2177-2317 2558-3332 3786-4298 4772-6123 6194-6228 6690-7175 7848-8485 8500-9065 9164-9476 9639-9771 9810-10055 11647-11771 11783-12245 13870-14332
HYAAH23	42	1032585	AL158156	1815	1-4481
HYAAH23	42	1032585	AL158155	1816	1-4477
HAJAV28	45	948630	AL121579	1817	1-175 1520-1889 2329-2473 2730-2805 3231-3444 4096-4273 7815-7900 8874-9058
HCE1S21	49	671209	AC007666	1818	1-122 274-371

					3724-3890 4511-4668 5669-6372 6679-7654
HCE1S21	49	671209	AC000052	1819	1-122 274-371 1127-1238 3724-3890 4511-4668 5669-6372 6679-7654
HCE1S21	49	671209	AC004019	1820	1-122 274-371 1127-1238 3724-3890 4511-4668 5669-6372 6679-7654
HCE1S21	49	671209	AC007666	1821	1-269 324-413
HCE1S21	49	671209	AC007666	1822	1-591 2367-2471 4522-4940 4990-5100 6036-6133 6225-6754 7871-7959 8764-9481
HCE1S21	49	671209	AC000052	1823	1-269 324-413
HCE1S21	49	671209	AC000052	1824	1-591 2366-2473
HCE1S21	49	671209	AC004019	1825	1-269 324-413
HCE1S21	49	671209	AC004019	1826	1-462
HCE3J64	50	951228	AC061705	1827	1-77 614-729 917-1028 1154-1218 1398-1591 1704-1802 2419-3315
HCFL154	52	921382	AC023278	1828	1-1977 2006-3504 3802-4090 4113-6041 6143-6242 6252-6919

					6933-7614 7682-8351
HCFLI54	52	921382	AC005562	1829	1-3490 3783-4087 4094-6238 6249-6901 6930-7364 7701-8350
HCFLI54	52	921382	AC023278	1830	1-574 774-1443
HCFLI54	52	921382	AC023278	1831	1-616
HCFLI54	52	921382	AC005562	1832	1-667
HCWDL45	55	889416	AC023100	1833	1-1181
HCWDL45	55	889416	Z98747	1834	1-1181
HDPGQ74	59	691163	AC073462	1835	1-173 1923-2056 2270-2362 4504-5101 5444-5630 6218-6268 8466-8542 8816-8888 10396-10437
HDPGS68	60	752975	AC034180	1836	1-950
HE2FR50	64	508498	AC010408	1837	1-574 1043-1729 1759-1995 2866-3391 3406-3626 3954-4396 4444-4667 5413-5515 8692-8774 8878-9828 13011-13373 14082-14365 15285-16319
HEBGK01	67	963673	Z97653	1838	1-627 815-1256 2165-2714
HEBGK01	67	963673	Z97653	1839	1-146
HEBGK01	67	963673	Z97653	1840	1-487
HEFMB30	68	691516	AC016659	1841	1-862
HEFMB30	68	691516	AC012481	1842	1-862
HEFMB30	68	691516	AC016659	1843	1-447
HEFMB30	68	691516	AC012481	1844	1-447
HEOPE58	69	851009	AL078634	1845	1-40 1089-1226

					3206-3637 4312-4463 7455-8330 8603-8815 9078-9190 9522-9767 10946-12260 13754-14357 15092-15830 18660-18822 21128-21635 21685-21721
HEOPE58	69	851009	AL078634	1846	1-235 3051-3154 3199-3734
HEOPE58	69	851009	AL078634	1847	1-444
HLHDD45	75	942901	AC024148	1848	1-116 629-787 1238-1305 1825-1969 2522-2966 2984-6238
HLHDD45	75	942901	AC069253	1849	1-116 629-787 1238-1305 1824-1968 2521-2965 2983-5879
HLHDD45	75	942901	AC044892	1850	1-116 629-787 1238-1305 1824-1968 2521-2965 2983-6236
HLHDD45	75	942901	AC044892	1851	1-105
HLHDD45	75	942901	AC069253	1852	1-105
HNHEQ86	79	785580	AC024653	1853	1-731
HSICX21	88	531267	AC016333	1854	1-552
HSICX21	88	531267	AC024101	1855	1-551
HSICX21	88	531267	AC016333	1856	1-448
HSICX21	88	531267	AC024101	1857	1-447
HSODC08	91	966264	AC005332	1858	1-1096 1112-1196 2142-2580 2893-3071 3148-3485 4737-5087 6182-6336

					6503-6667 7642-8422 8767-9265
HSODC08	91	966264	AC005332	1859	1-205 221-693
HSODC08	91	966264	AC005332	1860	1-181
HSQCM85	93	963554	AL021918	1861	1-629
HTOIA82	94	844319	AC012446	1862	1-410
HTOIA82	94	844319	AC012446	1863	1-329
HUUDH57	95	931155	AC009073	1864	1-118 2843-2982 5373-5675 6891-7201 8485-8641 9497-9900 10048-10506 10621-11749 12563-12695 12919-13053 14526-14766 16311-16378 17695-17869 18462-18541 19565-19750 21028-21485 25002-26608 26801-28071 28114-28369 28825-28998 29505-29648 31878-31961 32637-32809 32835-32936 33645-35911
HWAFFW39	97	947915	AC008508	1865	1-124 2706-3000 3745-3882 5914-6036 6110-6413 6491-6844 6912-7681 8888-9020 10437-10570 10686-11022
HWAFFW39	97	947915	AC008955	1866	1-544 2059-2219 2947-3088 5596-5891

					6635-6773 8782-8904 8978-9281 9359-9712 9778-10496
HWAFW39	97	947915	AC008963	1867	1-124 2645-2940 3685-3822 5831-5953 6027-6330 6408-6761 6828-7597 8806-8938 10353-10487 10603-10939 12315-12471 13563-13693 14450-14528 15001-16291
HWAFW39	97	947915	AC009073	1868	1-240 2827-3055 4160-4703 6218-6382 7102-7248 9770-10061 10805-10943 12952-13074 13148-13451 13529-13882 13951-14720 15927-16059 17474-17607 17723-18059 19435-19592 20686-20816 21573-21651 22124-23668 24035-24199 24212-24595 24879-25065 25816-26017 26260-26422 26424-26555 26824-27350 27380-27598 27609-27697 29321-29822 30645-30922

					31155-31244 31552-35653 35933-36067 36391-38070 38077-38991 39063-39584 40088-40196 40614-40660 41408-41837 41924-42048 42066-42712 42745-42876 43068-43760 43825-44062 44913-46162 46311-47285 47523-47779 50015-50221 50441-50512 50601-50653 50832-51143 52660-53226 53353-53439 53447-53826 53936-54038 57264-57491 59462-59560
HWAFFW39	97	947915	AC009073	1869	1-452
HWAFFW39	97	947915	AC008955	1870	1-229
HWAFFW39	97	947915	AC008963	1871	1-146
HBGDA14	114	866258	AC074220	1872	1-919
HBGDA14	114	866258	AC024580	1873	1-682
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HSYDB42	646	933545	AL022318	2313	1-156 1369-1531 1988-2167 2802-3008 3540-3823 4045-6131
HSYDB42	646	933545	AL022318	2314	1-492
HSYDB42	646	933545	AL022318	2315	1-407 1173-1467 1693-1857
HBGSS51	651	954855	AC012615	2316	1-607 763-1910 2291-2402 2983-3588 4170-4242
HBGSS51	651	954855	AC012615	2317	1-451
HBGSS51	651	954855	AC012615	2318	1-2083 2996-3117 3196-3330 3338-3638 3847-4160 4362-4596 5559-6225 6740-7087 7196-7297 7410-7746 7903-8059 8362-8495 8982-9518 10231-10522 11163-11210

[50] Table 1B summarizes additional polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) contig nucleotide sequence identifiers (SEQ ID NO:X)), and genomic sequences (SEQ ID NO:B). The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence. The second column provides the sequence identifier, "SEQ ID NO:X", for each contig sequence. The third column provides a unique contig identifier, "Contig ID:" for each contig sequence. The fourth column, provides a BAC identifier "BAC ID NO:A" for the BAC clone referenced in the corresponding row of the table. The fifth column provides the nucleotide sequence identifier, "SEQ ID NO:B" for a fragment of the BAC clone identified in column four of the corresponding row of the table. The sixth column, "Exon From-To", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:B which delineate certain polynucleotides of the invention that are also exemplary members of polynucleotide sequences that encode polypeptides of the invention (e.g., polypeptides containing amino acid sequences encoded by the polynucleotide sequences delineated in column six, and fragments and variants thereof).

TABLE 2

Clone ID NO:Z	Contig ID:	SEQ ID NO:X	Analysis Method	PFam/NR Description	PFam/NR Accession Number	Score/ Percent Identity	NT From	NT To
HHMMC14	1152250	11	blastx.2	GLYOXYLATE REDUCTASE (EC 1.1.1.79).	sp Q9UBQ7 Q9UBQ 7	96%	105	1088
HHMMC14	969371	652	HMMER 1.8	PFAM: D-isomer specific 2-hydroxyacid dehydrogenases	PF00389	217.83	336	965
			blastx.14	(AF146018) hydroxypyruvate reductase [Homo sapiens]	gi 5639830 gb AAD4 5886.1 AF146018_1	96%	87	1070
HSLEQ79	1184946	12	blastx.2	D-lactate dehydrogenase (EC 1.1.1.28) - Escherichia coli	pir G64888 G64888	93%	674	156
HSLEQ79	752382	653	HMMER 2.1.1	PFAM: D-isomer specific 2-hydroxyacid dehydrogenases	PF00389	222	19	453
HUCME08	1082023	13	blastx.2	GLYOXYLATE REDUCTASE (EC 1.1.1.79).	sp Q9UBQ7 Q9UBQ 7	88% 100%	110 54	625 107
HUCME08	868780	654	HMMER 2.1.1	PFAM: D-isomer specific 2-hydroxyacid dehydrogenases	PF00389	93.4	275	556
HNGOW33	1152254	14	blastx.2	8-amino-7-oxononanoate synthase (EC 2.3.1.47) - Escherichia coli	pir D32025 SYECKP	91% 70%	547 336	1158 497

HNGOW33	957351	655	HMMER 2.1.1 blastx.14	PFAM: Aminotransferases class-II (AE000195) orf, hypothetical protein [Escherichia coli]	PF00222	441.9	409	1251
HT4GD03	1103896	15	blastx.2	2-AMINO-3- KETOBUTYRATE COENZYME A LIGASE, MITOCHONDRIAL 1	sp O75600 KBL_HU MAN	93% 100%	153 89	968 166
HT4GD03	923731	656	HMMER 1.8 blastx.14	PFAM: Aminotransferases class-II dJ466N1.2 (2-amino-3- ketobutyrate-CoA ligase mRNA, 1	PF00222	78.93	575	877
HAQBZ89	949061	16	HMMER 1.8 blastx.2	PFAM: Aminotransferases class- III pyridoxal-phosphate	gi 4808241 emb CAB 42830.1	100% 87% 100%	584 153 140	967 569 166
HCCCC81	949062	17	HMMER 1.8 blastx.2	CG8745 PROTEIN. PFAM: Aminotransferases class- III pyridoxal-phosphate	sp Q9VU95 Q9VU95 PF00202	52% 178.37	8 187	316 816
HE8PW83	927532	18	HMMER 1.8 blastx.2	hypothetical protein T01B11.2 - Caenorhabditis elegans PFAM: Aminotransferases class- III pyridoxal-phosphate ALANINE-- GLYOXYLATE AMINOTRANSFERASE	pir T25848 T25848 PF00202	46% 139.27	190 4	879 465
					sp Q64565 AGT2_R AT	83%	4	546

HE9QQ22	949080	19	HMMER 2.1.1	2 PRECURSOR (EC 1.1 PFAM: Aminotransferases class- III pyridoxal-phosphate	PF00202	105.1	285	545
			blastx.2	ALANINE-- GLYOXYLATE AMINOTRANSFERASE 2 PRECURSOR (EC 1.1	sp Q64565 AGT2_R AT	51% 43% 49%	3 545 682	1070 1003 999
HFPFB39	946170	20	HMMER 1.8	PFAM: Aminotransferases class- III pyridoxal-phosphate	PF00202	235.05	1613	714
			blastx.2	hypothetical protein T01B11.2 - Caenorhabditis elegans	pir T25848 T25848	49%	1613	651
HSDJI44	1151680	21	blastx.2	adenosylmethionine--8- amino-7-oxononanoate transaminase (EC 2.6.1.62) - Escherichia coli	pir F64813 XNECDP	96%	857	2143
HSDJI44	974784	657	HMMER 2.1.1	PFAM: Aminotransferases class- III pyridoxal-phosphate	PF00202	511.4	894	1835
			blastx.14	(AE000180) 7,8- diaminopelargonic acid synthetase [Escherichia coli]	gi 1786991 gb AAC7 3861.1	99% 100%	795 1837	1841 1860
HE9DG38	1181748	22	blastx.2	Putative selenocysteine lyase.	sp AAF36816 AAF36 816	99%	44	994
HE9DG38	943384	658	HMMER 2.1.1	PFAM: Aminotransferases class-	PF00266	215.1	160	1326

				V					
				blastx.14	similar to NIFS protein (nitrogen fixation) [Caenorhabditis elegans]	gi 722379 gb AAC46 685.1	45% 53% 61% 46% 41% 57% 41%	442 877 724 1210 1081 313 1379	678 1038 840 1344 1209 375 1450
HGBAT24		1024746	23	blastx.2	phosphoserine transaminase (EC 2.6.1.52) - Escherichia coli	pir B64830 B64830	97%	1	369
HGBAT24		761143	659	HMMER 2.1.1	PFAM: Aminotransferases class- V	PF00266	128.3	10	369
HTDAF92		1181747	24	blastx.2	CDNA FLJ10515 FIS, CLONE NT2RP2000764, WEAKLY SIMILAR TO I	sp BAA91659 BAA9 1659	100%	256	1011
HTDAF92		943385	660	HMMER 2.1.1	PFAM: Aminotransferases class- V	PF00266	104.6	163	597
				blastx.2	(AF175767) putative selenocysteine lyase [Homo I	gb AAF36816.1 AF1 75767_1	100%	160	627
HAPSI19		668405	25	HMMER 1.8	PFAM: Cytochrome C and Quinol oxidase polypeptide I	PF00115	75.81	263	382
				blastx.2	cytochrome-c oxidase (EC 1.9.3.1) chain I - human	pir A00463 ODHU1	76% 95%	3 263	263 382

HADTU18	666268	26	HMMER 1.8 blastx.2	mitochondrion PFAM: Cytochrome C oxidase subunit II cytochrome-c oxidase (EC 1.9.3.1) chain II - human mitochondrion	PF00116 pir A00472 OBHU2	50% 100% 99.8 48%	28 385 185 2	87 399 307 436
HNTEF53	954852	27	HMMER 1.8 blastx.2	PFAM: Cytochrome P450	PF00067	102.61	369	887
HWLLB11	954849	28	HMMER 1.8 blastx.2	prostaglandin omega- hydroxylase (EC 1.14.15.-) cytochrome 1	pir S32315 A29368	49% 42% 60%	821 279 1705	1714 902 1749
			HMMER 1.8 blastx.2	PFAM: Cytochrome P450	PF00067	159.13	75	506
HCRQK86	1193068	29	HMMER 2.1.1 blastx.14	CYTOCHROME P450 4C3 (EC 1.14.14.1) (CYP1VC3).	sp Q9VA27 Q9VA27	46% 44%	78 4	512 75
HCRQK86	918014	662	HMMER 2.1.1 blastx.14	PROTEIN PHOSPHATASE 2C. PFAM: Protein phosphatase 2C (AF095927) protein phosphatase 2C [Rattus norvegicus]	sp Q9Z1Z6 Q9Z1Z6 PF00481	95% 248.4	164 467	1339 1297
HOCOT88	933635	30	HMMER 2.1.1 blastx.2	PFAM: Protein phosphatase 2C protein phosphatase 2C- like protein - Arabidopsis thaliana	gi 3777604 gb AAC9 7497.1 PF00481	89% 196.9	149 643	1324 1350
HELEF11	926930	31	HMMER	PFAM: Pyridoxal-	pir T50783 T50783 PF00282	38% 202.9	619 146	1371 565

		2.1.1	dependent decarboxylase conserved domain						
		blastx.2	glutamate decarboxylase (EC 4.1.1.15) beta - Escherichia coli	pir B43332 B43332	81% 100% 56% 47%	131 45 595 564	721 152 780 620		
HOUGD29	1204714	32	PANCREAS-ENRICHED PHOSPHOLIPASE C.	sp Q9UHV3 Q9UHV3	97% 79%	202 3	1821 203		
HOUGD29	909797	663	PFAM: Phosphatidylinositol-specific phospholipase C, Y domain	PF00387	118.2	202	453		
		blastx.14	(AF044576) phospholipase C PLC210 [Caenorhabditis elegans]	gi 2957270 gb AAC38963.1	42% 35% 58%	202 757 168	753 873 203		
HSIGN57	910078	33	PFAM: Phosphatidylinositol-specific phospholipase C, Y domain	PF00387	159.3	131	484		
		blastx.2	PHOSPHOLIPASE C-L2.	sp Q9QYGI Q9QYGI	83%	2	754		
HTEPE35	948475	34	PFAM: Phosphatidylinositol-specific phospholipase C, Y domain	PF00387	163.8	839	507		
		blastx.2	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase 1	pir S14113 S14113	48%	839	90		
HUFDB74	1227205	35	PHOSPHOINOSITIDE-SPECIFIC	sp Q91423 Q91423	60%	2	547		

						PHOSPHOLIPASE C (FRAGMENT).					
HUFDB74	901451	664		HMMER 2.1.1		PFAM: Phosphatidylinositol- specific phospholipase C, Y domain	PF00387	89.4	2	127	
HBXAB33	1229908	36		blastx.2		growth/differentiation factor 5 - human	pir JC2347 JC2347	98%	54	581	
HBXAB33	957228	665		HMMER 2.1.1 blastx.14		PFAM: Aminotransferases class-I aspartate aminotransferase precursor (2.6.1.1) [Homo sapiens]	PF00155 gi 179104 gb AAA35 568.1	663.4 95%	2286 2370	1081 1081	
HMAFB84	1198479	37		blastx.2		1- AMINOCYCLOPROPAN E-CARBOXILATE SYNTHASE.	sp Q9W698 Q9W698	54%	770	1462	
HMAFB84	944629	666		HMMER 1.8 blastx.14		PFAM: Aminotransferases class-I (AF108420) 1- aminocyclopropane- carboxylate synthase [Fugu rubripes]	PF00155 gi 4426837 gb AAD2 0564.1	37.62 58% 43%	55 1 452	429 447 499	
HPTVF17	1150836	38		blastx.2		1- AMINOCYCLOPROPAN E-CARBOXILATE SYNTHASE.	sp Q9W698 Q9W698	57% 59%	188 574	565 759	
HPTVF17	936688	667		HMMER 1.8 blastx.2		PFAM: Aminotransferases class-I (AF108420) 1-	PF00155 gb AAD20564.1	37.58 52%	275 188	607 679	

HSDIC55	1197407	39	blastx.2	aminocyclopropane-carboxylate synthase [Fugu rubripes]	pir A00598 XNECD	96%	115	345
HSDIC55	506582	668	HMMER 1.8	PFAM: Aminotransferases class-I	PF00155	97.17	106	363
HSDIL35	1228138	40	blastx.2	aspartate transaminase (EC 2.6.1.1) - Escherichia coli	pir A00598 XNECD	98%	2	226
HSDIL35	656370	669	HMMER 2.1.1	PFAM: Aminotransferases class-I	PF00155	195.1	3	371
HTXSM05	1104951	41	blastx.2	alanine transaminase (EC 2.6.1.2), cytosolic - human	pir A40465 A40465	67% 70%	5 456	406 515
HTXSM05	958447	670	HMMER 1.8	PFAM: Aminotransferases class-I	PF00155	38.39	23	316
			blastx.14	alanine aminotransferase [Homo sapiens]	gi 1507680 dbj BAA01186.1	66%	5	358
HYAAH23	1032585	42	blastx.2	GLYOXYLATE REDUCTASE (EC 1.1.1.79).	sp Q9UBQ7 Q9UBQ7	92%	1	606
HTPDX13	1134372	43	blastx.2	CARBOXYPEPTIDASE X2.	sp O54860 O54860	88%	2	922
HTPDX13	948419	671	HMMER 1.8	PFAM: Zinc carboxypeptidases	PF00246	87.75	257	682
			blastx.14	(AF017639) carboxypeptidase X2 [Mus musculus]	gi 2921092 gb AAC04670.1	88%	2	922

HAIHE43	1172244	44	blastx.2	NEURONAL THREAD PROTEIN AD7C-NTP.	sp O60448 O60448	41%	2538	1981
						38%	2289	1927
						48%	2186	1974
						40%	2446	2273
						38%	2510	2355
						56%	1963	1889
						41%	2541	2452
HAIHE43	966830	672	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	4.22	275	322
HAIJAV28	948630	45	HMMER 2.1.1	PFAM: Actin	PF00022	35.9	120	230
			blastx.2	Uncharacterized hypothalamus protein HARP11.	sp AAF67655 AAF67 655	97%	96	458
HAPOR59	712955	46	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	6.42	102	146
			blastx.2	CG5336 PROTEIN.	sp Q9VKB2 Q9VKB 2	40%	3	347
HBIBF78	772797	673	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	3.63	60	101
HCDAJ15	557243	674	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	3.61	68	88
HCE1S21	671209	49	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	4.17	163	210
			blastx.2	hypothetical protein F55G1.5 - Caenorhabditis elegans	pir T29225 T29225	60%	41	124
						43%	224	292
HCE3I64	951228	50	HMMER 2.1.1	PFAM: Peptidase family M13	PF01431	154.1	234	563
			blastx.2	ENDOTHELIN-	sp O60344 ECE2_HU	94%	3	599

HCFCV92	934216	675	HMMER 1.8	CONVERTING ENZYME 2 (EC 3.4.24.71) (ECE-2) 1 PFAM: Zinc-binding metalloprotease domain	MAN PF00099	59%	557	688
HCFLI54	921382	52	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	6.41	457	504
HCFND04	1155680	53	blastx.2	hypothetical protein ZK328.4 - Caenorhabditis elegans	pir T29006 T29006	28%	187	1134
HCFND04	873441	676	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	5.29	834	881
HCHMV63	666798	677	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	5.78	86	133
HCWDL45	889416	55	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	4.63	121	168
HCWEI19	1125258	56	blastx.2	alcohol dehydrogenase (EC 1.1.1.1) C - Escherichia coli (isolate VU 3685)	pir S57525 S57525	93%	215	436
HCWEI19	948690	678	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	8.6	226	273
			blastx.14	formaldehyde dehydrogenase (glutathione) [Escherichia coli]	gi 887431 emb CAA5 2057.1	75%	300	10
HCWKB72	1224131	57	blastx.2	SER/ARG-RELATED NUCLEAR MATRIX PROTEIN.	sp O60585 O60585	67% 52% 100% 38%	2613 1482 2049 2637	2921 1808 2108 2744

HCWKB72	676007	679	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	29%	2613	2795
HDDAF49	1125713	58	blastx.2	hypothetical protein DKFZp434D0215.1 - human (fragment)	pir T42650 T42650	58% 33%	912 202	2625 2744
HDDAF49	911314	680	HMMER 1.8 blastx.2	PFAM: Zinc-binding metalloprotease domain (AL133047) hypothetical protein [Homo sapiens]	PF00099 emb CAB61374.1	5.07 52%	144 9	173 269
HDPGQ74	691163	59	HMMER 1.8 blastx.2	PFAM: Zinc-binding metalloprotease domain TTYH1.	PF00099 sp AAG02580 AAG0 2580	3.86 44%	195 320	236 3
HDPGS68	752975	60	HMMER 1.8 blastx.2	PFAM: Zinc-binding metalloprotease domain ORF2-LIKE PROTEIN (FRAGMENT).	PF00099 sp O00549 O00549	6.96 37%	208 370	246 2
HDPIX67	1172240	61	blastx.2	CDNA FLJ20378 FIS, CLONE KAI0536.	sp BAA91131 BAA9 1131	65% 60%	1936 2115	2124 2183
HDPIX67	954385	681	HMMER 2.1.1	PFAM: Queuine tRNA- ribosyltransferase	PF01702	40.7	86	325

HDPXN01	915919	682	blastx.14	(AE000733) queuine tRNA-ribosyltransferase [Aquifex aeolicus]	gi 2983726 gb AAC0 7288.1	35%	86	313
HDQFT77	1136137	63	HMMER 1.8 blastx.2	PFAM: Zinc-binding metalloprotease domain KU70-BINDING PROTEIN (FRAGMENT).	PF000099 sp Q9Y6H3 Q9Y6H3	4.29 95%	99 98	146 958
HDQFT77	932212	683	HMMER 1.8 blastx.14	PFAM: Zinc-binding metalloprotease domain (AF078164) Ku70- binding protein [Homo sapiens]	PF000099 gi 4867999 gb AAD3 1085.1 AF078164_1	13.41 95%	496 13	534 873
HE2FR50	508498	64	HMMER 1.8 blastx.2	PFAM: Zinc-binding metalloprotease domain hypothetical protein DKFZp547N213.1 - human (fragment)	PF000099 pir T50613 T50613	3.68 79%	137	166 355
HE2SN25	948687	684	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF000099	9.04	227	268
HE8AE26	851514	685	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF000099	5.8	49	75
HEBGK01	963673	67	HMMER 1.8 blastx.2	PFAM: Zinc-binding metalloprotease domain C380A1.2.1 (NOVEL PROTEIN (ISOFORM 1)).	PF000099 sp Q9UJH9 Q9UJH9	4.13 81% 85% 100%	426 441 743 540	391 112 540 502
HEFMB30	691516	68	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF000099	4.57	144	185
HEOPE58	851009	69	HMMER	PFAM: Zinc-binding	PF000099	5.32	320	364

				1.8	metalloprotease domain				
HETBR74	948667	70		HMMER 2.1.1 blastx.2	PFAM: Rhodanese-like domain DUAL SPECIFICITY PROTEIN PHOSPHATASE 8 (EC 3.1.3.48) (EC 1 PRO1722..	PF00581	32.2	321	461
HFCAG94	1111177	71		blastx.2		sp O09112 DUS8_M OUSE	42% 54% 55%	291 458 535	476 523 588
HFCAG94	735763	686		HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	sp AAF69605 AAF69 605	66% 62%	860 1008	711 850
HFPHR82	957528	72		HMMER 2.1.1 blastx.2	PFAM: Actin Uncharacterized hypothalamus protein HARP11.	PF00099 PF00022 sp AAF67655 AAF67 655	3.92 91.7 100%	100 1322 1523	129 357 273
HHFOO84	857780	73		HMMER 1.8 blastx.2	PFAM: Zinc-binding metalloprotease domain	PF00099	4.21	141	161
HISAM68	1125189	74		blastx.2	CDNA FLJ20356 FIS, CLONE HEP15821.	sp BAA91112 BAA9 1112	100%	299	75
HISAM68	868785	687		HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	3.48	178	198
HLHDD45	942901	75		HMMER 1.8 blastx.2	PFAM: Zinc-binding metalloprotease domain	PF00099	5.88	177	218
HMMAB49	1087684	76		blastx.2	CDNA FLJ20378 FIS, CLONE KAIA0536.	sp BAA91131 BAA9 1131	60% 80%	678 464	466 402
HMMAB49	462502	688		HMMER 1.8 blastx.2	PFAM: Zinc-binding metalloprotease domain	PF00099	3.49	166	183
HMSGO27	683031	77		blastx.2	Unnamed portein product.	sp BAB01630 BAB0 1630	57% 68%	77 295	238 369

HMSGO27	943946	689	HMMER 2.1.1	PFAM: Reprolysin (M12B) family zinc metalloprotease	PF01421	59%	228	293
			blastx.2	(AF137335) metalloprotease disintegrin cysteine-rich protein, secreted form MDC-Ls [Homo sapiens]	gb AAD25100.1	92% 98% 35%	232 18 2	462 245 103
HNHAM52	457010	691	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	3.5	72	89
HNHEQ86	785580	79	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	3.9	7	48
HNHFF46	859822	692	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	5.55	3	35
HOECV83	653276	693	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	4.67	360	389
HORBO54	870674	82	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	5.64	277	300
HOSFZ73	913876	694	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	4.29	335	355
HPIAU71	1123830	84	blastx.2	ethanolamine ammonia- lyase (EC 4.3.1.7) heavy chain - Escherichia coli (strain K-12)	pir H65018 H65018	98% 79% 38%	400 104 578	68 3 516
HPIAU71	786811	695	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	3.49	265	291
HRDBT72	1112136	85	blastx.2	PRO1722.	sp AAF69605 AAF69 605	73% 75% 57%	821 673 609	666 614 532

HRDBT72	507847	696	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	7.31	295	324
HSDFT51	1124582	86	blastx.2	AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) 1	sp O09175 AMPB_R AT	33%	1291	872
HSDFT51	947918	697	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	6.14	328	363
HSDJM56	948669	87	blastx.14	aminopeptidase-B [Rattus norvegicus]	gi 1754515 dbj BAA1 3413.1	31% 36%	94 289	309 420
			HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	6.46	114	149
HSICX21	531267	88	blastx.2	formate C- acetyltransferase (EC 2.3.1.54) 1 - Escherichia coli	pir S01788 S01788	99% 99%	811 395	395 3
			HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	3.8	307	336
HSIDS82	531248	89	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	5.91	206	238
HSNAH21	571314	90	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	7.14	91	135
HSODC08	966264	91	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	14.78	551	510
			blastx.2	BM-014.	sp AAF64270 AAF64 270	94%	779	222
HSPAB58	736098	92	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	4.6	39	86
HSQCM85	963554	93	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	5.37	187	231
HTOLA82	844319	94	HMMER	PFAM: Zinc-binding	PF00099	4.25	50	82

HUUDH57	931155	95	1.8 HMMER 2.1.1 blastx.2	metallopeptidase domain PFAM: Peptidase family M1	PF01433	378.5	23	661
				ADIPOCYTE-DERIVED LEUCINE AMINOPEPTIDASE.	sp Q9UKY2 Q9UKY 2	51%	2	2155
HWACV74	1145916	96	blastx.2	CDNA FLJ20378 FIS, CLONE KAI0536.	sp BAA91131 BAA9 1131	52%	1731	1525
HWACV74	662347	698	HMMER 1.8	PFAM: Zinc-binding metallopeptidase domain	PF00099	4.43	198	242
HWAFW39	947915	97	HMMER 2.1.1 blastx.2	PFAM: Peptidase family M1	PF01433	79.5	200	367
				ADIPOCYTE-DERIVED LEUCINE AMINOPEPTIDASE.	sp Q9UKY2 Q9UKY 2	96%	200	367
HWBBR65	1156447	98	blastx.2	NEURONAL THREAD PROTEIN AD7C-NTP.	sp O60448 O60448	48%	1246	866
						63%	1150	971
						54%	703	539
						78%	791	708
						50%	791	618
						55%	1113	985
						38%	840	532
						48%	994	803
						62%	2216	2130
						37%	995	753
						60%	682	614
						34%	703	560
						63%	2241	2176
						57%	767	711
						84%	2215	2177

								32%	972	796
								47%	1129	1061
								46%	2183	2100
								40%	606	532
								37%	625	521
								71%	2140	2099
HWBBER65	747723	699	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099			4.15	185	205
HWMES65	969190	99	HMMER 2.1.1 blastx.2	PFAM: Matrixin	PF00413			45.6	17	109
				HATCHING ENZYME PRECURSOR (EC 3.4.24.12) (HE) (HEZ) 1	sp P91953 HE_HEM PU			51%	2	304
HISBG28	920850	100	HMMER 2.1.1 blastx.2	PFAM: 3'5'-cyclic nucleotide phosphodiesterase	PF00233			195.7	187	789
				3'5'-cyclic-AMP phosphodiesterase (EC 3.1.4.-) - human (fragment)	pir A47286 A47286			90%	1	804
HAAJAE60	786337	101	HMMER 2.1.1 blastx.2	PFAM: Aconitase family (aconitate hydratase)	PF00330			72.2	228	353
				ACONITATE HYDRATASE, MITOCHONDRIAL PRECURSOR (EC 4.2.1.3) (CITRATE HYDRO-LYASE) (ACONITASE).	sp Q99798 ACON_H UMAN			61%	15	353
HDPDE32	1217181	102	blastx.2	aconitate hydratase (EC	pir G64875 G64875			91%	69	887

HDPDE32	973342	700	HMMER 2.1.1	4.2.1.3) - Escherichia coli PFAM: Aconitase family (aconitate hydratase)	PF00330	260.7	219	569
HBDAC79	1199232	103	blastx.2	ACYL-COENZYME A DEHYDROGENASE-8 PRECURSOR (CDNA FLJ20352 FIS, CLONE HEP14524).	sp Q9UKU7 Q9UKU 7	86% 97% 45%	196 3 452	528 203 583
HBDAC79	935414	701	HMMER 2.1.1	PFAM: Acyl-CoA dehydrogenase	PF00441	102.6	94	342
			blastx.14	(AL021958) fadE9 [Mycobacterium tuberculosis]	gi 2911026 emb CAA 17519.1	62% 51% 64% 35%	94 250 348 6	255 384 422 89
HEMDX48	1163778	104	blastx.2	ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC, 1	sp P50544 ACDV_M OUSE	48%	175	1917
HEMDX48	521844	702	HMMER 1.8	PFAM: Acyl-CoA dehydrogenases	PF00441	115.91	4	321
HHASB48	721150	105	HMMER 2.1.1	PFAM: Acyl-CoA dehydrogenase	PF00441	101.3	319	645
			blastx.2	ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC, 1	sp P50544 ACDV_M OUSE	54%	175	648
HLWCA17	1104762	106	blastx.2	probable acyl-CoA dehydrogenase PA2550 [imported] - Pseudomonas aeruginosa (strain PAO1)	pir D83326 D83326	62%	359	979

HLWCA17	957664	703	HMMER 1.8	PFAM: Acyl-CoA dehydrogenases	PF00441	52.61	521	892
			blastx.14	(AL096811) putative acyl-CoA dehydrogenase [Streptomyces coelicolor A3(2)]	gi 5441764 emb CAB46788.1	53% 58%	521 286	904 519
HNTTD09	1104487	107	blastx.2	K09H11.1 PROTEIN.	sp O01590 O01590	47% 32%	179 6	832 152
HNTTD09	676665	704	HMMER 1.8	PFAM: Acyl-CoA dehydrogenases	PF00441	49.76	60	425
HSKDT07	927823	108	HMMER 1.8	PFAM: Acyl-CoA dehydrogenases	PF00441	122.42	13	369
			blastx.2	ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC, 1	sp P50544 ACDV_MOUSE	38%	7	906
HSRDB26	1102231	109	blastx.2	acyl CoA dehydrogenase homolog - Escherichia coli	pir I41124 I41124	99% 72% 81%	305 27 2	658 305 34
HSRDB26	525475	705	HMMER 2.1.1	PFAM: Acyl-CoA dehydrogenase	PF00441	115.7	21	290
HAPBS07	967325	110	HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	50.05	61	267
			blastx.2	RETINOL DEHYDROGENASE HOMOLOG.	sp Q9Y2P9 Q9Y2P9	75% 69% 62% 34%	317 61 580 561	682 306 708 683
HAUAI17	921674	111	HMMER 2.1.1	PFAM: short chain dehydrogenase	PF00106	198.7	172	687

			blastx.2	RETINAL SHORT-CHAIN DEHYDROGENASE/REDUCTASE RETSDR3.	sp Q9UKU3 Q9UKU3	81% 100%	145 687	687 857
HBCBT19	959953	112	HMMER 2.1.1	PFAM: short chain dehydrogenase	PF00106	30.7	202	417
			blastx.2	hypothetical protein F17A8.100 - Arabidopsis thaliana	pir T04022 T04022	40% 41% 52%	214 38 591	552 196 653
HBCPT10	957631	113	HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	98.87	338	673
			blastx.2	CDNA FLJ11008 FIS, CLONE PLACE1003100, MODERATELY SIMILAR 1	sp BAA91953 BAA91953	97% 80%	263 671	670 838
HBGDA14	866258	114	HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	127.15	3	299
			blastx.2	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase (EC 1.3.1.28) - Escherichia coli	pir A91904 DEECDB	92%	3	482
HCHNJ32	934848	115	HMMER 2.1.1	PFAM: short chain dehydrogenase	PF00106	213.6	54	587
			blastx.2	CARBONYL REDUCTASE.	sp Q9UHY9 Q9UHY9	95%	33	764
HCHON59	931082	116	HMMER 2.1.1	PFAM: SCP-2 sterol transfer family	PF02036	96.3	1006	1335

HCUGN19	716989	117	blastx.2	CG5590 PROTEIN.	sp Q9VB10 Q9VB10	47%	538	1344
			HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	68%	99	536
HCUGR38	706471	118	HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	8.05	98	151
			blastx.2	Putative oxidoreductase.	sp CAB94622 CAB94622	73.02	102	284
						55%	105	296
						30%	4	81
HDPND85	852628	119	HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	191.2	113	709
			blastx.2	CG9360 PROTEIN.	sp Q9VYU9 Q9VYU9	42%	113	841
						175.59	123	680
HDPRN38	883658	120	HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106			
			blastx.2	Peroxisomal trans 2-enoyl CoA reductase (EC 1.3.1.8).	sp AAF69798 AAF69798	81%	111	824
						84%	61	138
HE8AM92	952610	121	HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	8.98	202	330
			blastx.2	DTDP-4-KETO-6-DEOXY-D-GLUCOSE 4-REDUCTASE.	sp Q9UJ54 Q9UJ54	90%	208	654
HE9RE21	888243	122	HMMER 2.1.1	PFAM: short chain dehydrogenase	PF00106	81.3	96	386
			blastx.2	ESTRADIOL 17 BETA-	sp P56937 DHB7 H	100%	90	419

HETKH30	884009	123		DEHYDROGENASE 7 (EC 1.1.1.62) 1	UMAN	88%	421	522
			HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	137.09	300	881
			blastx.2	PUTATIVE STEROID DEHYDROGENASE SPM2 (EC 1.1.1.-).	sp O57314 DHBX_A NAPL	54%	294	866
HHAME78	840939	124	HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	55.01	60	260
			blastx.2	CARBONYL REDUCTASE.	sp Q9UHY9 Q9UHY 9	83% 100% 95% 81%	48 322 257 2	260 426 322 67
			HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	11.34	109	285
HKABI68	856590	125	blastx.2	HSCARG.	sp AAG09721 AAG0 9721	99% 75%	139 456	441 551
			HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	100.69	23	361
			blastx.2	STEROID DEHYDROGENASE HOMOLOG.	sp Q9Y6G8 Q9Y6G8	98%	20	583
HMCFA91	959954	127	HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	25.77	19	282
			blastx.2	hypothetical protein	pir T04022 T04022	53%	367	648

HNTBF75	836701	128	HMMER 2.1.1 blastx.2	F17A8.100 - Arabidopsis thaliana PFAM: short chain dehydrogenase STEROID DEHYDROGENASE HOMOLOG.	PF00106 sp Q9Y6G8 Q9Y6G8	41%	1	282
HPTGB43	726460	129	HMMER 2.1.1 blastx.2	PFAM: short chain dehydrogenase CARBONYL REDUCTASE.	PF00106 sp Q9UHY9 Q9UHY 9	45.1 73%	84 87	191 374
HPTVL90	509487	130	HMMER 2.1.1 blastx.2	PFAM: short chain dehydrogenase RETINAL SHORT- CHAIN DEHYDROGENASE/RE DUCTASE RETSDR3.	PF00106 sp Q9UKU3 Q9UKU 3	46.3 76%	11 8	115 319
HSKIA89	837986	131	HMMER 1.8 blastx.2	PFAM: Alcohol/other dehydrogenases, short chain type hypothetical protein T11F9.11 - Caenorhabditis elegans	PF00106 pir T24832 T24832	17.7 42% 53% 35%	359	478 619 320 820
HTXGF27	695766	132	HMMER 2.1.1 blastx.2	PFAM: short chain dehydrogenase hypothetical protein DKFZp566O084.1 - human	PF00106 pir T17307 T17307	208.7 93% 100%	193 70 38	765 1011 73
HWHHW54	684125	133	HMMER 2.1.1	PFAM: short chain dehydrogenase	PF00106	59.1	871	1002

				blastx.2	Oxidoreductase UCPA.	sp AAF80754 AAF80754	77%	871	1059
HWHP029	857383	134		HMMER 2.1.1 blastx.2	PFAM: short chain dehydrogenase CGI-82 PROTEIN.	PF00106 sp Q9Y391 Q9Y391	101.3 74% 64%	257 257 186	664 664 260
HWLPR94	967326	135		HMMER 1.8 blastx.2	PFAM: Alcohol/other dehydrogenases, short chain type RETINOL DEHYDROGENASE HOMOLOG.	PF00106 sp Q9Y2P9 Q9Y2P9	44.2 95% 84%	193 184 36	417 450 134
HWLUL28	925331	136		HMMER 1.8 blastx.2	PFAM: Alcohol/other dehydrogenases, short chain type C359F1.1 (novel protein (ortholog of mouse and rat 1	PF00106 sp CAB92744 CAB92744	113.24 82%	163 97	588 735
HWLXT48	957630	137		HMMER 1.8 blastx.2	PFAM: Alcohol/other dehydrogenases, short chain type CDNA FLJ11008 FIS, CLONE PLACE1003100, MODERATELY SIMILAR 1	PF00106 sp BAA91953 BAA91953	46.57 83% 94%	133 58 309	306 333 359
HBGMD15	1103922	138		blastx.2	L-threonine 3-dehydrogenase (EC 1.1.1.103) - Escherichia coli	pit A33276 DEECTH	91% 79%	64 554	564 655
HBGMD15	786307	706		HMMER	PFAM: Zinc-binding	PF00107	141.1	3	323

HNGMA91	789744	139	2.1.1 HMMER 1.8 blastx.2	dehydrogenases PFAM: Zinc-binding dehydrogenases probable alcohol dehydrogenase (EC 1.1.1.1) ybdR - Escherichia coli	PF00107	28.74	76	231
HSLEI57	1103672	140	blastx.2	alcohol dehydrogenase (EC 1.1.1.1) C - Escherichia coli	pir D64763 D64763	87%	74	565
HSLEI57	730927	707	HMMER 2.1.1	PFAM: Zinc-binding dehydrogenases	PF00107	236	5	388
HSLFE21	1103524	141	blastx.2	probable oxidoreductase (EC 1.1.1.-) ycjQ - Escherichia coli	pir D64880 D64880	95%	2	994
HSLFE21	823083	708	HMMER 1.8 blastx.2	PFAM: Zinc-binding dehydrogenases probable alcohol dehydrogenase (EC 1.1.1.1) ybdR - Escherichia coli	PF00107	76.21	344	655
HSLJE40	1105422	142	blastx.2	PFAM: Zinc-binding dehydrogenases	pir F64794 F64794	97%	88	510
HSLJE40	866274	709	HMMER 1.8	PFAM: Zinc-binding dehydrogenases	PF00107	30.97	152	283
HTXHA35	1152110	143	blastx.2	CGI-63 PROTEIN.	sp Q9Y373 Q9Y373	98% 72%	309 14	836 190
HTXHA35	633682	710	HMMER 1.8	PFAM: Zinc-binding dehydrogenases	PF00107	53.56	265	471
HAICS07	1105538	144	blastx.2	ALDO-KETO REDUCTASE.	sp O09125 O09125	75% 75% 63%	193 535 733	480 738 798

HAICS07	953351	711	HMMER 2.1.1	PFAM: Aldo/keto reductase family	PF00248	283	193	480
			blastx.14	aldo-keto reductase [Mus musculus]	gi 1698718 gb AAB3 7274.1	76% 75% 91%	193 535 733	480 738 768
HBKDN33	1167313	145	blastx.2	Acetyl-CoA synthetase.	sp AAF75064 AAF75 064	85% 85%	2 955	1015 1014
HBKDN33	922414	712	HMMER 2.1.1	PFAM: AMP-binding enzyme	PF00501	249.5	2	931
			blastx.14	acetyl-CoA synthetase [Drosophila melanogaster]	gi 608694 emb CAA8 6738.1	65%	2	1222
HBODH62	1228278	146	blastx.2	DJ568C11.3 (novel AMP- binding enzyme similar to 1	sp CAB75500 CAB7 5500	98% 100%	344 297	1696 362
HBODH62	742827	713	HMMER 1.8	PFAM: AMP-binding enzymes	PF00501	43.02	27	158
HCEPJ44	1157810	147	blastx.2	Sequence 17 from Patent WO9951740.	sp CAC07591 CAC0 7591	99%	2	571
HCEPJ44	930790	714	HMMER 1.8	PFAM: AMP-binding enzymes	PF00501	19.17	3	215
			blastx.14	(AF023258) fatty acid transport protein [Mus musculus]	gi 2612939 gb AAC6 9640.1	90%	9	536
HCWCM65	1105668	148	blastx.2	probable non-ribosomal peptide synthetase PA2402 [imported] - Pseudomonas aeruginosa (strain PAO1)	pir F83345 F83345	75% 74% 37% 31% 57% 53%	12 12 9 9 595 595	611 611 605 596 678 678
HCWCM65	529230	715	HMMER	PFAM: AMP-binding	PF00501	69.62	31	264

HDQDY52	1182322	149	1.8 blastx.2	enzymes DJ18C9.1 (SIMILAR TO ACETYL-COENZYME A SYNTHETASE) 1	sp Q9UJ15 Q9UJ15	84% 81% 55%	85 566 705	690 778 785
HDQDY52	852622	716	HMMER 1.8 blastx.2	PFAM: AMP-binding enzymes (AL049709) dJ18C9.1 (similar to acetyl- coenzyme A synthetase) [Homo sapiens]	PF00501 emb CAB61786.1	82.8	316	555
HEEA32	1203140	150	blastx.2	CDNA FLJ20581 FIS, CLONE REC00491.	sp BAA91273 BAA9 1273	93% 97% 57%	502 3 1146	1182 500 1208
HEEA32	887490	717	HMMER 1.8	PFAM: AMP-binding enzymes	PF00501	35.92	39	407
HEGAN70	839719	151	HMMER 1.8 blastx.2	PFAM: AMP-binding enzymes Hypothetical 179.7 kDa protein.	PF00501 sp AAF64300 AAF64 300	18.6 61% 85% 34% 54%	334 124 31 295 748	516 654 111 579 846
HFKMF42	1104119	152	blastx.2	Long-chain-fatty-acid- CoA ligase-like protein.	sp BAB02683 BAB0 2683	48% 41%	656 65	1096 556
HFKMF42	923824	718	HMMER 1.8 blastx.14	PFAM: AMP-binding enzymes 4-coumarate-coA ligase [Mycobacterium leprae]	PF00501 gi 699196 gb AAA62 961.1	91.1 51% 48% 55% 36% 50%	86 764 647 365 968 491	901 949 781 484 1099 568

HFPHG06	1104964	153	blastx.2	enterobactin synthetase component F - Escherichia coli	pir H64791 YGECEF	53% 44%	65 570	103 623
HFPHG06	933802	719	HMMER 2.1.1 blastx.14	PFAM: AMP-binding enzyme enterobactin [Escherichia coli]	PF00501 gi 145843 gb AAA92015.1	66 90%	53 2	232 220
HHEMB89	1227613	154	blastx.2	DJ568C11.3 (novel AMP-binding enzyme similar to 1)	sp CAB75500 CAB75500	99%	561	1961
HHEMB89	574897	720	HMMER 2.1.1	PFAM: AMP-binding enzyme	PF00501	115.4	1	453
HLDPC46	466567	155	HMMER 1.8 blastx.2	PFAM: AMP-binding enzymes CDNA FLJ20581 FIS, CLONE REC00491.	PF00501 sp BAA91273 BAA91273	103.84 89% 57%	17 17 586	481 571 681
HLDRG44	1106225	156	blastx.2	KIDNEY-SPECIFIC PROTEIN.	sp O70490 O70490	74%	16	1011
HLDRG44	969544	721	HMMER 1.8 blastx.14	PFAM: AMP-binding enzymes (AF062389) kidney-specific protein [Rattus norvegicus]	PF00501 gi 3127193 gb AAD05209.1	104.64 78%	89 2	694 931
HLICR73	1107517	157	blastx.2	VERY LONG-CHAIN ACYL-COA SYNTHETASE HOMOLOG 2.	sp Q9Y2P5 Q9Y2P5	96%	9	536
HLICR73	837030	722	HMMER	PFAM: AMP-binding	PF00501	20.33	19	324

			1.8	enzymes				
			blastx.2	(AF064255) very long-chain acyl-CoA synthetase homolog 2; VLCS-H2 [Homo sapiens]	gb AAD29444.1 AF064255_1	99% 100%	1 450	441 497
HNHOP64	1103943	158	blastx.2	FATTY ACID TRANSPORT PROTEIN.	sp O95186 O95186	90% 52%	515 57	57 1
HNHOP64	966754	723	HMMER 1.8	PFAM: AMP-binding enzymes	PF00501	23.65	539	757
			blastx.14	(AF055899) fatty acid transport protein [Homo sapiens]	gi 4206376 gb AAD11623.1	88% 52%	374 835	835 891
HSDEF56	1128288	159	blastx.2	acetate--CoA ligase (EC 6.2.1.1) - Escherichia coli	pir D65215 D65215	97% 95% 100%	106 707 897	729 892 986
HSDEF56	496551	724	HMMER 2.1.1	PFAM: AMP-binding enzyme	PF00501	175.3	2	436
HTENI29	1105518	160	blastx.2	LONG-CHAIN ACYL-COA SYNTHETASE 5.	sp Q9UKU0 Q9UKU0	97%	24	1172
HTENI29	954519	725	HMMER 1.8	PFAM: AMP-binding enzymes	PF00501	65	366	845
			blastx.14	(AF129166) long-chain acyl-CoA synthetase 5 [Homo sapiens]	gi 5702202 gb AAD47199.1 AF129166_1	98%	51	1172
HWMKD72	1106729	161	blastx.2	agmatinase PA1421 [imported] - Pseudomonas aeruginosa (strain PAO1)	pir H83468 H83468	64%	2	643
HWMKD72	970613	726	HMMER 2.1.1	PFAM: Arginase family	PF00491	179.6	11	565
			blastx.14	agmatine ureohydrolase	gi 882466 gb AAA69	48%	302	625

				[Escherichia coli]	104.1]		50%	14	166
HAPSQ21	972037	162	HMMER 2.1.1	PFAM: Eukaryotic aspartyl protease	PF00026		44%	164	271
			blastx.2	NAPSIN 1 PRECURSOR (EC 3.4.23.-) (NAPSIN A) (NAPA) 1	sp O96009 NAP1_H UMAN		274.4	211	735
HLJDW02	1192885	163	blastx.2	NAPSIN 1 PRECURSOR (EC 3.4.23.-) (NAPSIN A) (NAPA) 1	sp O96009 NAP1_H UMAN		100%	58	762
							90%	767	865
HLJDW02	837592	727	HMMER 2.1.1	PFAM: Eukaryotic aspartyl protease	PF00026		134.5	65	412
			blastx.2	(AF090386) napsin A [Homo sapiens]	gb AAD04917.1		100%	47	433
							65%	433	534
HMGBT01	1205666	164	blastx.2	aspartic proteinase (EC 3.4.23.-) BACE precursor - human	pir A59090 A59090		100%	3	1073
							85%	1705	1992
HMGBT01	879904	728	HMMER 1.8	PFAM: Eukaryotic aspartyl proteases	PF00026		31.46	3	362
HSSJJ24	1178041	165	blastx.2	aspartic proteinase (EC 3.4.23.-) BACE precursor - human	pir A59090 A59090		100%	8	1081
							85%	1714	2001
HSSJJ24	905092	729	HMMER 1.8	PFAM: Eukaryotic aspartyl proteases	PF00026		26.48	33	113
HFTCG46	669383	166	HMMER 2.1.1	PFAM: Eukaryotic-type carbonic anhydrase	PF00194		101.7	78	266
			blastx.2	CARBONIC ANHYDRASE VB, MITOCHONDRIAL PRECURSOR (EC 1	sp Q9Y2D0 CA5B_H UMAN		98%	78	257

HNTMD81	929511	167	HMMER 2.1.1 blastx.2	PFAM: Eukaryotic-type carbonic anhydrase CARBONIC ANHYDRASE XIV PRECURSOR (EC 4.2.1.1) (CARBONATE 1 OUTER MEMBRANE USHER PROTEIN PMFC PRECURSOR.	PF00194 sp Q9ULX7 CAHE_ HUMAN	84.3	16	249
						69%	19	369
						69%	135	437
						90%	434	499
HBSAJ60	1174334	168	blastx.2	PFAM: Citrate synthase	sp Q9R7S7 Q9R7S7	99%	2043	2885
						97%	2888	3331
HBSAJ60	573965	730	HMMER 2.1.1	PFAM: Citrate synthase	PF00285	192	2	265
HSKCI43	506599	169	HMMER 1.8	PFAM: Citrate synthase	PF00285	69.36	1	315
			blastx.2	citrate (si)-synthase (EC 4.1.3.7) - Escherichia coli	pir G64807 YKEC	64%	1	345
						96%	168	260
HSDKE47	1128095	170	blastx.2	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain NDUF52 precursor - human	pir JE0193 JE0193	100%	73	195
HSDKE47	764970	731	HMMER 2.1.1	PFAM: Respiratory-chain NADH dehydrogenase, 49 Kd subunit	PF00346	79.8	64	195
HCWTB56	1172460	171	blastx.2	probable cation- transporting P-type ATPase PA2435 [imported] - Pseudomonas aeruginosa (strain PAO1)	pir F83342 F83342	65%	2	268
						95%	270	332
HCWTB56	853009	732	HMMER 1.8	PFAM: E1-E2 ATPases	PF00122	55.15	2	301
			blastx.2	cadmium resistance	gb AAB37345.1	42%	2	316

HFPBS73	1144027	172	blastx.2	protein [Lactococcus lactis] H+/K+-exchanging ATPase (EC 3.6.1.36) chain B [validated] - Escherichia coli	pir H64804 PWECB K	81%	373	1122
HFPBS73	954892	733	HMMER 2.1.1 blastx.2	PFAM: E1-E2 ATPase kdpB [Escherichia coli]	PF00122 gb AAB96336.1	196.5 100% 100%	3 580	572 563 603
HOEDD44	954893	173	HMMER 2.1.1 blastx.2	PFAM: E1-E2 ATPase H+/K+-exchanging ATPase (EC 3.6.1.36) chain B [validated] - Escherichia coli	PF00122 pir H64804 PWECB K	173.2 92% 96% 39%	53 53 634 513	574 574 723 635
HSUAN33	956315	174	HMMER 1.8 blastx.2	PFAM: E1-E2 ATPases Hypothetical 128.8 kDa protein.	PF00122 sp CAB89728 CAB8 9728	46.29 48% 35%	1317 1596 693	907 766 256
HBCMD49	1206021	175	blastx.2	hypothetical protein F38H4.8 - Caenorhabditis elegans	pir T21981 T21981	44%	46	357
HBCMD49	865314	734	HMMER 2.1.1 blastx.2	PFAM: Enoyl-CoA hydratase/isomerase family (AE000989) enoyl-CoA hydratase (fad-4) [Archaeoglobus fulgidus]	PF00378 gb AAB89601.1	74.6 39%	263 197	550 619
HKABN12	956826	176	HMMER	PFAM: Enoyl-CoA	PF00378	31.8	900	820

HMOAC31	1228291	177		2.1.1 blastx.2	hydatase/isomerase family CG6984 PROTEIN.	sp Q9V7Y3 Q9V7Y3	37% 41%	745 891	593 739
	1228291	177		blastx.2	probable 3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157) ydbU - Escherichia coli (strain K-12)	pir F64890 F64890	93%	1297	2586
HMOAC31	920386	735		HMMER 2.1.1	PFAM: Enoyl-CoA hydratase/isomerase family	PF00378	159.1	5	268
				blastx.14	enoyl-CoA hydratase [Escherichia coli]	gi 2764828 emb CAA66095.1	88% 90%	2 334	355 495
HMVBQ92	1204710	178		blastx.2	CDNA FLJ10948 FIS, CLONE PLACE1000142, WEAKLY SIMILAR TO 1	sp BAA91922 BAA91922	99%	1701	2090
HMVBQ92	791284	736		HMMER 1.8	PFAM: Enoyl-CoA hydratase/isomerase	PF00378	32.87	167	274
HOELA62	1228151	179		blastx.2	CDNA FLJ10948 FIS, CLONE PLACE1000142, WEAKLY SIMILAR TO 1	sp BAA91922 BAA91922	98%	1685	2074
HOELA62	863712	737		HMMER 2.1.1	PFAM: Enoyl-CoA hydratase/isomerase family	PF00378	39.5	1635	1757
HSSGE35	1228152	180		blastx.2	CDNA FLJ10948 FIS, CLONE PLACE1000142,	sp BAA91922 BAA91922	89%	97	498

					WEAKLY SIMILAR TO					
HSSGE35	967832	738	HMMER 1.8 blastx.14		PFAM: Enoyl-CoA hydratase/isomerase AU-binding protein/Enoyl-CoA hydratase [Homo sapiens]	PF00378	39.59	70	210	
HEMFJ74	1216651	181	blastx.2		GLUCOSAMINE-- FRUCTOSE-6- PHOSPHATE AMINOTRANSFERASE 1 1	gi 780241 emb CAA5 6260.1 sp O94808 GFA2_H UMAN	57% 55% 69% 100% 98%	88 1 363 193 1301	357 87 401 1299 1468	
HEMFJ74	523350	739	HMMER 2.1.1		PFAM: Glutamine amidotransferases class-II	PF00310	74.1	124	348	
HISCL24	676997	182	HMMER 2.1.1 blastx.2		PFAM: Glutamine amidotransferases class-II GLUCOSAMINE-- FRUCTOSE-6- PHOSPHATE AMINOTRANSFERASE 1 1	PF00310 sp O94808 GFA2_H UMAN	92.7 85%	3 3	233 560	
H7PBB83	1228150	183	blastx.2		CG9630 PROTEIN.	sp Q9VHU1 Q9VHU 1	47% 56% 25%	145 955 776	774 1044 871	
H7PBB83	908235	740	HMMER 1.8 blastx.14		PFAM: Helicases conserved C-terminal domain (AJ010469) RNA helicase [Arabidopsis thaliana]	PF00271 gi 3776011 emb CAA 09208.1	84.64	756	586	
HAGBA63	1122199	184	blastx.2		PUTATIVE ATP-	sp O43630 O43630	99%	1121	78	

HAGBA63	509775	741	HMMER 1.8	DEPENDENT MITOCHONDRIAL RNA HELICASE.	PF00271	7.62	2	124
HBMUG47	1102698	185	blastx.2	PFAM: Helicases conserved C-terminal domain	sp Q9UNC8 Q9UNC8	98%	21	530
HBMUG47	863846	742	HMMER 1.8	RECQ HELICASE 5 (DNA HELICASE RECQ5 GAMMA).	PF00271	52.06	22	204
HCRPZ84	1130816	186	blastx.2	PFAM: Helicases conserved C-terminal domain	sp AAG09428 AAG09428	37% 25% 34% 40%	3 1469 1161 834	893 1942 1640 1013
HCRPZ84	965476	743	HMMER 1.8	RNA helicase.	PF00271	13.09	923	1063
			blastx.14	PFAM: Helicases conserved C-terminal domain	gi 4405795 gb AAD19826.1	45% 43% 59% 50% 56% 45% 30% 44%	137 506 26 1063 413 863 737 1154	373 622 91 1140 460 934 853 1228
HCWTR54	1192287	187	blastx.2	(AF038963) RNA helicase [Homo sapiens]	sp O60448 O60448	64% 69% 48%	304 245 313	179 120 233

HCWTR54	729290	744	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	27% 85%	331 364	233 344
HDPBB41	1195686	188	blastx.2	RNA helicase HEL117 - rat	pir A57514 A57514	90% 88% 45%	2411 2722 2814	564 2372 2545
HDPBB41	925800	745	HMMER 2.1.1	PFAM: Helicases conserved C-terminal domain	PF00271	108.7	47	292
HEOPI32	907903	189	blastx.14 HMMER 1.8	(AF106680) RNA helicase [Homo sapiens] PFAM: Helicases conserved C-terminal domain	gi 5410326 gb AAD4 3033.1 PF00271	82% 89.44	17 176	637 430
HFSAG03	1151479	190	blastx.2	DJ620E11.1A (NOVEL HELICASE C- TERMINAL DOMAIN AND SNF2 1 1 PRO0478.	sp Q9UIF0 Q9UIF0	87%	2	661
HFSAG03	960973	746	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	sp Q9UI59 Q9UI59 PF00271	67% 6.39	967 454	1086 365
HFXCI24	1182719	191	blastx.2	probable ATP-dependent RNA helicase rhIE - Escherichia coli	pir E64816 E64816	81%	12	674
HFXCI24	908374	747	HMMER 2.1.1	PFAM: Helicases conserved C-terminal domain	PF00271	128.5	151	396

HFXHJ89	907938	192	blastx.14 HMMER 1.8	Putative ATP-dependent RNA helicase RhIE. [Escherichia coli] PFAM: Helicases conserved C-terminal domain	gi 4062355 dbj BAA3 5457.1 PF00271	94% 100%	1 644	543 664
			blastx.2	DJ620E11.1A (NOVEL HELICASE C- TERMINAL DOMAIN AND SNF2 1 1	sp Q9UUF0 Q9UUF0	98% 78% 48%	210 37 5	881 207 85
HHPTC55	1106390	193	blastx.2	hypothetical protein C27B7.4 - Caenorhabditis elegans	pir T19508 T19508	47%	2	541
HHPTC55	907951	748	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	61.91	13	243
			blastx.14	(AF026032) ATRX protein [Mus musculus]	gi 3002558 gb AAC0 8741.1	54%	4	351
HJBBS4	1195070	194	blastx.2	DJ616B8.1 (RNA HELICASE) (Fragment).	sp CAC03449 CAC0 3449	89%	3	551
HJBBS4	869621	749	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	10.61	3	170
			blastx.2	(AC005314) putative pre- mRNA splicing factor RNA helicase [Arabidopsis thaliana]	gb AAC36188.1	54%	3	563
HKAHB56	1162649	195	blastx.2	RNA helicase.	sp AAG09428 AAG0 9428	28% 31% 33%	833 333 54	1606 824 389

HKAHB56	865298	750	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	63.37	699	986
HLDCE35	1151490	196	blastx.2	APOBEC-1 stimulating protein.	sp CAB94754 CAB9 4754	83%	84	725
HLDCE35	831356	751	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	6.01	288	374
			blastx.2	(AF209192) Apobec-1 complementation factor [Homo 1	gb AAF34824.1 AF2 09192_1	94%	177	725
HMCBU79	1165318	197	blastx.2	CDNA FLJ20110 FIS, CLONE COL05103.	sp BAA90955 BAA9 0955	89%	1	987
HMCBU79	856630	752	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	17.95	349	459
HNTRV07	1199546	198	blastx.2	Cytoplasmic dynein heavy chain.	sp BAA97048 BAA9 7048	92% 91% 40%	934 18 48	2001 923 152
HNTRV07	952794	753	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	6.41	274	345
			blastx.14	similar to dynein heavy chain; cDNA EST EMBL:D27549.1 [Caenorhabditis elegans]	gi 3876099 emb CAA 99830.1	33%	46	333
HODEX10	926260	754	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	9.2	22	54
HOGAQ10	1222600	200	blastx.2	Proliferation-associated	sp AAF82262 AAF82	99%	1045	1992

HOGAQ10	907911	755	HMME 1.8	SNF2-like protein. PFAM: Helicases conserved C-terminal domain	262 PF00271	94%	98	1051
HOSBW20	985056	201	blastx.14	lymphocyte specific helicase [Mus musculus]	gi 805296 gb AAB08 015.1	93%	80	556
HOSBW20	668774	756	blastx.2 HMME 1.8	CG7972 PROTEIN. PFAM: Helicases conserved C-terminal domain	sp Q9VSE2 Q9VSE2 PF00271	83% 47% 13.94	18 4 58	71 777 96
HRADL60	1151310	202	blastx.2	probable pre-mRNA splicing factor ATP- dependent RNA helicase - fission yeast (Schizosaccharomyces pombe)	pir T37496 T37496	40% 42%	2750 2750	1416 1737
HRADL60	967578	757	HMME 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	14.84	248	496
HSGSC29	1150837	203	blastx.2	(AL009197) putative pre- mRNA splicing factor ATP-dependent RNA helicase [Schizosaccharomyces pombe]	emb CAA15715.1	40% 44%	83 83	1429 1096
HSGSC29	953599	758	blastx.2 HMME 1.8	ACTIN INTERACTING PROTEIN. PFAM: Helicases conserved C-terminal domain	sp O23240 O23240 PF00271	56% 9.31	334 345	750 446

				blastx.14	actin interacting protein [Arabidopsis thaliana]	gi 4006920 emb CAB 16815.1	53%	468	740
HTEDX38	1106208	204		blastx.2	DEAD-BOX PROTEIN.	sp Q9Y659 Q9Y659	70%	333	452
HTEDX38	920697	759		HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	90%	55	1494
							70.92	3	176
HTEJE15	1102531	205		blastx.14	(AF106019) DEAD-box protein [Homo sapiens]	gi 5359631 gb AAD4 2744.1 AF106019_1	90%	3	1436
				blastx.2	VASA protein.	sp AAF72705 AAF72 705	100%	1	405
HTEJE15	908360	760		HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	14.92	5	52
				blastx.14	vasa-like gene protein, RVLG protein=putative DEAD 1 [Rattus sp.]	gi 806464 gb AAB33 364.1	73%	2	190
							84%	242	319
							65%	188	265
HTOES03	1150877	206		blastx.2	TRANSCRIPTIONAL ACTIVATOR SRCAP.	sp Q9Y5L9 Q9Y5L9	40%	203	1186
HTOES03	955814	761		HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	53.97	240	491
				blastx.14	(AF143946) transcriptional activator SRCAP [Homo sapiens]	gi 5106572 gb AAD3 9760.1 AF143946_1	50%	6	569
							39%	906	1019
							33%	540	656
HTOHS18	1193057	207		blastx.2	ATP-DEPENDENT RNA HELICASE.	sp Q9SHB9 Q9SHB9	39%	39	857
HTOHS18	908347	762		HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	104.65	158	370
				blastx.14	(AC007660) putative	gi 4895231 gb AAD3	45%	23	439

HWAAX38	943936	208	HMMER 1.8	RNA helicase [Arabidopsis thaliana] PFAM: Helicases conserved C-terminal domain	2817.1 AC007660_18	47%	579	761
			blastx.2	PUTATIVE SNF2/SWI2 FAMILY TRANSCRIPTION FACTOR	sp Q9SHB2 Q9SHB2	46%	39	380
HMSFN70	1210794	209	blastx.2	CDNA FLJ20421 FIS, CLONE KAT02467.	sp BAA91158 BAA9 1158	96%	1	921
HMSFN70	921879	763	HMMER 2.1.1	PFAM: Inositol monophosphatase family	PF00459	40.2	703	795
			blastx.14	(AL032655) predicted using Genefinder; similar to 1 this gene [Caenorhabditis elegans]	gi 3881275 emb CAA 21725.1	43% 52% 48% 24%	328 703 556 25	492 822 678 273
HUSGB93	1224029	210	blastx.2	BISPHOSPHATE 3'- NUCLEOTIDASE.	sp O95861 O95861	99% 100%	426 146	953 364
HUSGB93	923014	764	HMMER 1.8	PFAM: Inositol monophosphatase family	PF00459	33.91	125	388
			blastx.14	(AF125042) bisphosphate 3-nucleotidase [Homo sapiens]	gi 4325316 gb AAD1 7329.1	100%	17	493
HELHL56	1164004	211	blastx.2	CDNA FLJ11068 FIS, CLONE PLACE1004918, WEAKLY SIMILAR TO 1	sp BAA91985 BAA9 1985	99%	8	655
HELHL56	578441	765	HMMER 1.8	PFAM: L-lactate dehydrogenases	PF00056	33.17	80	211

HOENY85	1191756	212	blastx.2	CDNA FLJ11068 FIS, CLONE PLACE1004918, WEAKLY SIMILAR TO 1	sp BAA91985 BAA9 1985	93%	53	1069
HOENY85	875830	766	HMMER 1.8	PFAM: L-lactate dehydrogenases	PF00056	144.25	38	598
HTEHI14	1102680	213	blastx.2	LACTATE DEHYDROGENASE A (EC 1.1.1.27).	sp Q9XT87 Q9XT87	68%	218	523
HTEHI14	526687	767	HMMER 2.1.1	PFAM: lactate/malate dehydrogenase	PF00056	50.6	222	371
HETDT70	1228235	214	blastx.2	NMD PROTEIN.	sp O95991 O95991	99% 52%	25 540	558 596
HETDT70	937999	768	HMMER 2.1.1	PFAM: Lipase	PF00151	125.4	139	528
			blastx.2	similar to the following EST sequences: GenBank Accession 1 sapiens]	gb AAC99994.1	88% 52%	25 539	597 595
HPIAT34	936262	215	HMMER 2.1.1	PFAM: Lipase	PF00151	123.9	305	535
			blastx.2	NMD PROTEIN.	sp O95991 O95991	80% 100% 92% 66%	266 84 12 277	574 275 95 330
HDPPO41	1204324	216	blastx.2	malate dehydrogenase (NAD+) (EC 1.1.1.-) precursor, mitochondrial - human	pir A39503 A39503	98%	186	1937
HDPPO41	963126	769	HMMER 2.1.1	PFAM: Malic enzyme	PF00390	243.6	258	572

HMSHI83	1204709	217	blastx.14	mitochondrial NAD(P)+ - dependent malic enzyme [Homo sapiens]	gi 187300 gb AAA36 197.1	99%	186	569
			blastx.2	malate dehydrogenase (NAD+) (EC 1.1.1.-) precursor, mitochondrial - human	pir A39503 A39503	98%	2	1720
HMSHI83	963083	770	HMMER 2.1.1	PFAM: Malic enzyme	PF00390	621.6	41	751
			blastx.14	mitochondrial NAD(P)+ - dependent malic enzyme. [Homo sapiens]	gi 187300 gb AAA36 197.1	96% 72% 43%	2 753 855	784 785 902
HTEPM45	952389	218	HMMER 2.1.1	PFAM: Malic enzyme	PF00390	924.1	33	1175
			blastx.2	malate dehydrogenase (NAD+) (EC 1.1.1.-) precursor, mitochondrial - human	pir A39503 A39503	97%	33	1229
HTEPM45	953366	771	HMMER 2.1.1	PFAM: Fibrillar collagen C-terminal domain	PF01410	561.6	286	939
			blastx.2	prepro-alpha-1 type 3 collagen [Homo sapiens]	emb CAA32583.1	100% 59% 54% 54% 54% 53% 54% 48% 50%	37 31 37 37 31 37 37 43 43	942 126 132 129 129 126 129 129 126
HE8OV13	1228507	219	blastx.2	myosin heavy chain	pir S51823 S51823	44%	33	923

HE8OV13	911341	772	HMMER 1.8 blastx.14	ATM2 - Arabidopsis thaliana (fragment) PFAM: Myosin head (motor domain) (contains ATP/GTP binding P-loop) myr 6 myosin heavy chain [Rattus norvegicus]	PF00063 gi 1575333 gb AAB3 8840.1	32%	1263	1484
HELGU27	1011928	220	blastx.2	MYOSIN I.	sp Q63357 Q63357	93% 100%	1 788	786 817
HELGU27	923702	773	HMMER 2.1.1 blastx.14	PFAM: Myosin head (motor domain) myosin I [Rattus norvegicus]	PF00063 gi 3724141 emb CAA 50871.1	256.3 97% 100% 100% 100%	8 11 688 662 719	640 640 717 676 736
HHEDC90	1226157	221	blastx.2	MYOSIN I.	sp Q63357 Q63357	57%	216	3263
HHEDC90	911447	774	HMMER 2.1.1 blastx.14	PFAM: Myosin head (motor domain) myosin I [Rattus norvegicus]	PF00063 gi 3724141 emb CAA 50871.1	241.2 67%	25 1	597 645
HNBREB59	685902	222	HMMER 1.8 blastx.2	PFAM: Myosin head (motor domain) (contains ATP/GTP binding P-loop) MYOSIN II NONMUSCLE (FRAGMENT).	PF00063 sp Q91300 Q91300	94.31 92%	85 85	243 246
HNNBI16	965414	223	HMMER 2.1.1	PFAM: Myosin head (motor domain)	PF00063	116.7	101	292

HUJCL61	1223496	224	blastx.2	myosin I gamma, MMI gamma - mouse (fragment) MYOSIN.I	pir C45438 C45438	49%	101	337
			blastx.2		sp Q63357 Q63357	59% 47% 41%	159 2698 364	2717 3207 414
HUJCL61	911432	776	HMMER 2.1.1	PFAM: Myosin head (motor domain)	PF00063	196	170	544
			blastx.14	myosin I [Rattus norvegicus]	gi 3724141 emb CAA50871.1	72% 55% 81%	140 604 534	532 750 599
HWLRC68	1089187	225	blastx.2	Myosin X (Fragment)	sp AAF36524 AAF36524	100% 92% 66%	90 1238 1267	1238 1276 1302
HWLRC68	911481	777	HMMER 2.1.1	PFAM: Myosin head (motor domain)	PF00063	97.7	222	485
HFXFH42	713795	778	HMMER 1.8	PFAM: Neuraminidases	PF00064	9.26	259	354
HEQAN73	958912	227	HMMER 2.1.1	PFAM: Phosphoglycerate mutase family	PF00300	64.2	87	359
			blastx.2	Hypothetical 30.1 kDa protein.	sp CAC01127 CAC01127	99%	69	878
HSLFS31	1106294	228	blastx.2	right oriC-binding protein - Escherichia coli	pir JU0158 JU0158	99%	566	252
HSLFS31	921511	779	HMMER 2.1.1	PFAM: Phosphoglycerate mutase family	PF00300	71.6	12	149
			blastx.14	Kenn Rudd identifies as gpmB [Escherichia coli]	gi 537235 gb AAA97291.1	96% 100%	3 188	188 223
HELK56	1103702	229	blastx.2	pyruvate kinase (EC 2.7.1.40) A - Escherichia	pir S29790 S29790	96% 63%	572 619	96 554

HELK56	925698	780	HMMER 2.1.1	coli PFAM: Pyruvate kinase	PF00224	406.9	147	731
			blastx.14	pyruvate kinase type II [Escherichia coli]	gi 147459 gb AAA24 473.1	98% 65%	147 21	731 107
HAMFW05	957586	230	HMMER 1.8	PFAM: Proyl oligopeptidase family	PF00326	33.83	1	174
			blastx.2	R26984_1 (FRAGMENT)	sp O75273 O75273	95%	1	558
HTEDG81	1193054	231	blastx.2	ALPHA 4 SUBUNIT OF 20S PROTEASOME.	sp Q9PTW9 Q9PTW 9	89%	79	771
HTEDG81	772995	781	HMMER 2.1.1	PFAM: Proteasome A- type and B-type	PF00227	114.6	180	488
HAMGO24	943287	232	HMMER 2.1.1	PFAM: Ribonucleotide reductases	PF00268	316.2	2	490
			blastx.2	hypothetical protein DKFZp761E1312.1 - human (fragment)	pir T46249 T46249	90%	2	550
HMWBH91	1193044	233	blastx.2	house-keeping protein - mouse	pir S27870 S27870	53% 52%	282 121	1295 279
HMWBH91	882083	782	HMMER 1.8	PFAM: Ribosomal RNA adenine dimethylases	PF00398	23.82	385	921
HOECH19	965639	234	HMMER 1.8	PFAM: Ribosomal RNA adenine dimethylases	PF00398	116.68	173	934
			blastx.2	CGI-75 PROTEIN.	sp Q9Y384 Q9Y384	95% 100% 100%	140 72 911	853 161 934
HSRAA80	1121919	235	blastx.2	POLYMERASE (FRAGMENT)	sp Q9UQG0 Q9UQG 0	63% 39%	17 421	361 498
HSRAA80	937640	783	HMMER	PFAM: Reverse	PF00078	20.88	11	130

			1.8	transcriptase (RNA-dependent DNA polymerase)					
			blastx.14	(AF080232) polymerase [Human endogenous retrovirus K]	gi 3600069 gb AAC63292.1	65%	17	325	
HHEDF50	1174682	236	blastx.2	nitrogen regulation protein II (EC 2.7.3.-) ntrB - Escherichia coli	pir A30377 RGECGL	89%	44	490	
HHEDF50	974396	784	HMMER 1.8	PFAM: Signal C terminal domain	PF00512	115.35	65	490	
			blastx.14	NR(II) (glnL gene product) (AA 1-349) [Escherichia coli]	gi 41564 emb CAA28807.1	100%	86	427	
HHEMK34	974395	237	HMMER 1.8	PFAM: Signal C terminal domain	PF00512	62.83	56	277	
			blastx.2	nitrogen regulation protein II (EC 2.7.3.-) ntrB - Escherichia coli	pir A30377 RGECGL	78%	50	415	
HMAGK69	1105451	238	blastx.2	hypothetical 60.6 kD protein in dcub-lysu intergenic region - Escherichia coli (strain K-12)	pir D65222 D65222	96% 100%	523 618	26 523	
HMAGK69	723186	785	HMMER 1.8	PFAM: Signal C terminal domain	PF00512	40.87	31	405	
HNGNW52	1132300	239	blastx.2	protein-histidine kinase (EC 2.7.3.-) - Escherichia coli	pir G64840 G64840	93% 80% 90%	939 86 37	55 42 5	
HNGNW52	883074	786	HMMER	PFAM: Signal C terminal	PF00512	174.7	464	997	

			1.8	domain				
H6EDK67	974775	240	HMIMER 2.1.1 blastx.2	PFAM: Signal peptidase I	PF00461	218.3	165	641
				signal peptidase (EC 3.4.99.-) 21K chain - dog	pir A34229 A34229	98%	93	668
HWBCS43	1151532	241	blastx.2	signal peptidase (EC 3.4.99.-) 18K chain - dog	pir A35309 A35309	93%	344	880
HWBCS43	772564	787	HMIMER 2.1.1	PFAM: Signal peptidase I	PF00461	117.2	381	653
HCE3H71	961681	242	HMIMER 2.1.1 blastx.2	PFAM: Sushi domain (SCR repeat) seizure-related protein SEZ-6 precursor - mouse	PF00084 pir I52657 I52657	79.2 83% 64% 30% 48%	317 5 565 98 929	496 685 957 496 1000
HOFMS43	947973	243	HMIMER 2.1.1 blastx.2	PFAM: Sushi domain (SCR repeat) PORCINE MEMBRANE COFACTOR PROTEIN.	PF00084 sp O02839 O02839	64 47%	174 12	302 317
HOVCO14	947999	244	HMIMER 2.1.1 blastx.2	PFAM: Sushi domain (SCR repeat) UNKNOWN PROTEIN (FRAGMENT).	PF00084 sp Q28797 Q28797	84 33% 34% 38% 47%	21 21 424 424	170 347 380 516 474
HTOBE75	1161571	245	blastx.2	P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) 1-MOLECULE 3)	sp P16109 LEM3_H UMAN	95% 38% 37% 35% 34%	3 3 3 3 3	1067 878 866 863 866

HTOBE75	591896	788	HMMER 2.1.1	(LECAM3). PFAM: Sushi domain (SCR repeat)	PF00084	39%	48	866
HCMSEL08	898203	246	HMMER 2.1.1 blastx.2	PFAM: Calsequestrin calsequestrin precursor, fast skeletal muscle - human	PF01216 pir A60424 A60424	100.1 95%	52 112	1221 1197
HCMSEL08	959176	789	HMMER 2.1.1 blastx.14	PFAM: Calsequestrin calmitine; calsequestrine [Homo sapiens]	PF01216 gi 688292 gb AAB32 063.1	697.4 93%	1372	569 593
HDPBS64	846624	247	HMMER 1.8 blastx.2	PFAM: Thioredoxins ZK973.11 protein.	PF00085 sp AAF40013 AAF40 013	116.87 32%	173 182	493 652
HDTBR50	846630	248	HMMER 1.8 blastx.2	PFAM: Thioredoxins NM23-H8.	PF00085 sp AAF20909 AAF20 909	29.85 100% 97%	163 130 327	297 327 467
HTDAB17	890384	249	HMMER 2.1.1 blastx.2	PFAM: Thioredoxin CG1837 PROTEIN.	PF00085 sp Q9VYV3 Q9VYV 3	107.9 42% 43% 41%	276 225 231 348	533 518 539 533
HABAE22	1227053	250	blastx.2	CARBOXY TERMINUS OF HSP70- INTERACTING PROTEIN.	sp Q9UNE7 Q9UNE7	95%	169	1023
HABAE22	965314	790	HMMER	PFAM: TPR Domain	PF00515	38.4	300	383

			2.1.1	(AF039689) antigen NY-CO-7 [Homo sapiens]	gi 3170178 gb AAC18038.1	92%	171	725
HE9MI70	1217048	251	blastx.2	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 25 (EC 3.1.2.15) 1 PROTEASE 25)	sp P57080 UBPP_MOUSE	52%	15	758
HE9MI70	953319	791	HMMER 1.8	(DEUBIQUITINATING ENZYME 25).	PF00515	16.42	154	240
HHFDK15	854734	792	HMMER 2.1.1	PFAM: TPR Domain	PF00515	21.7	213	299
HOSNZ11	1162664	253	blastx.2	conserved hypothetical protein MTH68 - Methanobacterium 1	pir E69190 E69190	36%	134	448
HOSNZ11	965875	793	HMMER 2.1.1	PFAM: TPR Domain	PF00515	30.3	144	230
			blastx.14	(AE000798) O-linked GlcNAc transferase [Methanobacterium thermoautotrophicum]	gi 2621106 gb AAB84576.1	34% 23% 36%	249 3 395	362 236 484
HTAEW05	1151514	254	blastx.2	DJ979N1.1 (DJ979N1.1).	sp Q9UGR2 Q9UGR2	100%	215	658
HTAEW05	838562	794	HMMER 1.8	PFAM: TPR Domain	PF00515	16.51	460	546
HTTKN45	1181807	255	blastx.2	BCDNA:GH04929 PROTEIN	sp Q9V3G6 Q9V3G6	23%	420	1583

HTTKN45	914589	795	HMMER 1.8	PFAM: TPR Domain	PF00515	18.74	383	469
			blastx.14	(AF181631) BcDNA.GH04929 [Drosophila melanogaster]	gi 5901818 gb AAD5 5417.1 AF181631_1	46% 26%	539 386	685 487
HUSJN62	923146	256	HMMER 2.1.1	PFAM: TPR Domain	PF00515	38.4	1075	992
			blastx.2	CARBOXY TERMINUS OF HSP70- INTERACTING PROTEIN.	sp Q9UNE7 Q9UNE7	94%	1189	353
HTEIU92	1102681	257	blastx.2	Transketolase (EC 2.2.1.1).	sp AAF76194 AAF76 194	71%	1	564
HTEIU92	870652	796	HMMER 2.1.1	PFAM: Transketolase	PF00456	70.1	1	225
HAQMD86	1105267	258	blastx.2	UBIQUITIN CARBOXYL- TERMINAL HYDROLASE 10 (EC 3.1.2.15) 1 1	sp Q14694 UBPA_H UMAN	96%	13	1878
HAQMD86	961459	797	HMMER 2.1.1	PFAM: Ubiquitin carboxyl-terminal hydrolase family 2	PF00443	89.1	1700	1900
			blastx.14	similar to ubiquitin- specific proteinase of S.cerevisiae. [Homo sapiens]	gi 1136438 dbj BAA1 1507.1	96%	2	1879
HBJJG02	1151462	259	blastx.2	CG5794 PROTEIN.	sp Q9VC56 Q9VC56	48%	795	1409
HBJJG02	919508	798	HMMER 2.1.1	PFAM: Ubiquitin carboxyl-terminal	PF00443	80.6	176	460

HBJJN65	blastx.14			hydrolase family 2	gi 1666075 emb CAA 66942.1	56%	164	253
				ubiquitin hydrolase [Homo sapiens]		26%	314	481
	blastx.2	260	UBIQUITIN CARBOXYL- TERMINAL HYDROLASE 25 (EC 3.1.2.15) 1 PROTEASE 25) (DEUBIQUITINATING ENZYME 25).	sp P57080 UBPP_M OUSE	55%	50	103	
					25%	485	613	
					25%	626	709	
					46%	281	319	
					31%	821	886	
					22%	188	268	
37%	5	541						
HBJJN65	HMMER 2.1.1	960507	799	PFAM: Ubiquitin carboxyl-terminal hydrolase family 2	PF00443	80.5	514	723
HBMUJ35	blastx.14			similar to ubiquitin carboxyl-terminal hydrolase; 1 1-cDNA EST EMBL:D64405 comes from this gene; cDNA EST EMBL:D68146	gi 3878110 emb CAA 87786.1	40%	409	588
						40%	607	681
HBMUJ35	blastx.2	1195500	261	UBIQUITIN CARBOXYL- TERMINAL HYDROLASE 23 (EC	sp Q9UK80 UBPN_H UMAN	91%	1982	288

HBMUJ35	956041	800	HMMER 2.1.1	3.1.2.15) 1 1 PFAM: Ubiquitin carboxyl-terminal hydrolase family 2	PF00443	54.6	492	355
			blastx.14	(AF177758) ubiquitin specific protease 16 [Homo sapiens]	gi 5853113 gb AAD5 4321.1 AF177758_1	98% 91%	627 359	355 288
HCEBP60	1227635	262	blastx.2	LSFR3 PROTEIN (FRAGMENT).	sp Q9W6U5 Q9W6U 5	85% 75%	1737 2863	2846 2910
HCEBP60	812297	801	HMMER 1.8	PFAM: Ubiquitin carboxyl-terminal hydrolases family 2	PF00443	59.49	168	281
HFGMA55	1150870	263	blastx.2	UBIQUITIN CARBOXYL- TERMINAL HYDROLASE 23 (EC 3.1.2.15) 1 1	sp Q9UK80 UBPN_H UMAN	100%	10	444
HFGMA55	858681	802	HMMER 2.1.1	PFAM: Ubiquitin carboxyl-terminal hydrolase family 2	PF00443	57.8	237	377
HLHTE91	789603	264	HMMER 2.1.1	PFAM: Ubiquitin carboxyl-terminal hydrolase family 2	PF00443	92.4	862	1068
			blastx.2	DEUBIQUITINATING ENZYME.	sp Q9UNP0 Q9UNP0	40%	409	1077
HLHTE91	868803	803	HMMER 2.1.1	PFAM: MYND finger	PF01753	33.7	393	521
HL YFI58	1151495	265	blastx.2	UBIQUITIN CARBOXYL- TERMINAL	sp Q9YST5 UBPG_H UMAN	100%	2	625

HL YFI58	924193	805	HMMER 2.1.1 blastx.14	HYDROLASE 16 (EC 3.1.2.15) 1 1 1 PFAM: Ubiquitin carboxyl-terminal hydrolase family 2 (AF126736) ubiquitin processing protease [Homo sapiens]	PF00443 gi 4454565 gb AAD2 0949.1	77.4 100%	368 2	619 625
HNNBJ44	915273	806	HMMER 2.1.1 blastx.14	PFAM: Ubiquitin carboxyl-terminal hydrolase family 2 similar to ubiquitin carboxyl-terminal hydrolase; 1 1 cDNA EST EMBL:D34547 comes from this gene; cDNA EST EMBL:D37684	PF00443 gi 3879501 emb CAA 87795.1	50.1 44% 28% 42% 35% 23% 72%	1045 688 292 1276 1093 1961 1057	1131 915 462 1332 1134 2062 1089
HSLJI46	997643	267	blastx.2	UBIQUITIN CARBOXYL- TERMINAL HYDROLASE 8 (EC 3.1.2.15) 1 1	sp P40818 UBP8_HU MAN	82% 100% 79%	64 1 510	498 87 596
HSLJI46	883028	807	HMMER 2.1.1 blastx.2	PFAM: Ubiquitin carboxyl-terminal hydrolase family 2 CG3016 PROTEIN.	PF00443 sp Q9W462 Q9W462	99.8 56% 41% 63.6	1336 361 16 359	1521 561 153 568
HTFOK70	1151518	268	blastx.2	PFAM: Ubiquitin carboxyl-terminal hydrolase family 2	PF00443			
HTFOK70	914561	808	HMMER 2.1.1	PFAM: Ubiquitin carboxyl-terminal hydrolase family 2				

HUSXO71	1164014	269	blastx.14	(AC003974) putative ubiquitin specific protease [Arabidopsis thaliana]	gi 2914695 gb AAC0 4485.1	60%	473	571
				UBIQUITIN CARBOXYL- TERMINAL HYDROLASE 18 (EC 3.1.2.15) 1 1 1	sp Q9UMW8 UBPI_ HUMAN	39%	7	129
						37%	368	472
						100%	400	480
HUSXO71	862649	809	HMMER 2.1.1	PFAM: Ubiquitin carboxyl-terminal hydrolase family 2	PF00443	65.2	1290	1505
HWBDP39	1223498	270	blastx.2	CDNA FLJ20314 FIS, CLONE HEP07831.	sp BAA91084 BAA9 1084	88%	1313	2239
HWBDP39	810403	810	HMMER 2.1.1	PFAM: Ubiquitin carboxyl-terminal hydrolase family 2	PF00443	55.2	227	382
HKMMQ73	840459	271	HMMER 1.8	PFAM: UDP- glucuronosyl and UDP- glucosyl transferases	PF00201	93.48	28	327
			blastx.2	2-hydroxyacylsphingosine 1-beta- galactosyltransferase (EC 1	pir JC5423 JC5423	88%	7	417
HVVBK72	1179755	272	blastx.2	glucuronosyltransferase (EC 2.4.1.17) UGT2B13 precursor - rabbit	pir B47113 B47113	35%	69	461
HVVBK72	933167	812	HMMER 1.8	PFAM: UDP- glucuronosyl and UDP- glucosyl transferases	PF00201	70.01	2	391
H7TXB52	981972	273	blastx.2	DUAL SPECIFICITY	sp Q9UNI6 DUSC_H	100%	303	1322

H7TXB52	910910	813	HMMER 2.1.1	PROTEIN PHOSPHATASE 12 (EC 3.1.3.48) (EC 1 PFAM: Dual specificity phosphatase, catalytic domain	UMAN PF00782	117.9	378	806
			blastx.14	(AB004537) PROTEIN- TYROSINE PHOSPHATASE YVH1 [Schizosaccharomyces pombe]	gi 2257526 dbj BAA2 1420.1	26% 48% 52% 38%	516 1143 1092 960	968 1292 1142 1013
HDPRY71	1217205	274	blastx.2	Mitogen-activated protein kinase phosphatase x.	sp AAF86649 AAF86 649	99% 100%	531 392	848 529
HDPRY71	971345	814	HMMER 2.1.1	PFAM: Dual specificity phosphatase, catalytic domain	PF00782	109.1	492	719
			blastx.14	DsPTP1 protein [Arabidopsis thaliana]	gi 4150963 emb CAA 77232.1	48% 43%	492 377	716 487
HGOCA12	968763	275	HMMER 2.1.1	PFAM: Dual specificity phosphatase, catalytic domain	PF00782	28.6	112	360
			blastx.2	PROTEIN PHOSPHATASE.	sp Q9UII6 Q9UII6	40%	25	360
HGOCA12	971583	815	HMMER 2.1.1	PFAM: Dual specificity phosphatase, catalytic domain	PF00782	60.1	467	318
			blastx.14	phosphatase tyrosine/serine [Homo sapiens]	gi 181840 gb AAA35 777.1	48%	515	318
HHJCJ29	1077517	276	blastx.2	hypothetical protein	pir T14756 T14756	100%	490	1716

					DKFZp564F0923.1 - human (fragment)				75%	1927	2073
									60%	208	402
									31%	128	412
									32%	146	520
									27%	137	508
									75%	3	50
									37%	212	403
HHCJ29	916885	816	HMMER 1.8	blastx.14	PFAM: Protein-tyrosine phosphatase (AL110210) hypothetical protein [Homo sapiens]	PF00102			63.32	50	244
HODGC61	973449	277	HMMER 1.8	blastx.2	PFAM: Protein-tyrosine phosphatase	PF00102			97%	5	436
HBXGQ52	1229467	278	blastx.2		glutamate--ammonia ligase (EC 6.3.1.2) - <i>Escherichia coli</i>	pir S40815 AJECQ			56%	492	539
									6.61	130	222
HBXGQ52	576093	817	HMMER 2.1.1	blastx.2	PFAM: Glutamine. synthetase	PF00120			100%	2	874
									166.6	1	270
HE2JS39	1121932	279	blastx.2		glutamine synthetase [<i>Escherichia coli</i>]	gb AAB3004.1			83%	1	360
									93%	101	721
HE2JS39	957854	818	HMMER 1.8	blastx.2	CHLORIDE INTRACELLULAR CHANNEL PROTEIN 3.	sp O95833 CLB3_HU MAN			20.49	75	647
HE7SH21	960302	280	HMMER 1.8	blastx.2	PFAM: Glutathione S- transferases.	PF00043			54.61	150	950
									93%	162	782
HMLAO23	1103488	281	blastx.2		DJ995J12.1 (similar to ganglioside-induced 1	sp CAB75497 CAB7 5497			88%	2	478

HMIAO23	675329	819	HMNER 2.1.1	INDUCED DIFFERENTIATION ASSOCIATED PROTEIN I.	PF00043	29.5	23	184
HELDW45	944301	282	HMNER 2.1.1	PFAM: Glutathione S- transferases.	PF00408	133.1	114	512
HSRBB31	1121889	283	blastx.2	Phosphoglucosyltransferase/phos phomannomutase	pir G64803 G64803	99%	3	512
HSRBB31	958210	820	blastx.2	phosphoglucosyltransferase (EC 5.4.2.2) - Escherichia coli	sp BAA99407 BAA9 9407	100% 64% 54% 71%	3 493 395 707	440 861 526 790
HTEOW39	1151517	284	HMNER 1.8	PFAM: Biotin-requiring enzymes	PF00364	75.97	1455	1643
HTEOW39	870566	821	HMNER 1.8	lysozyme (EC 3.2.1.17) - bare-faced crassow	pir JE0185 JE0185	49%	65	484
HE2PE32	1106571	285	blastx.2	PFAM: C-type lysozymes and alpha-lactalbumin	PF00062	126.92	59	295
HE2PE32	524511	822	HMNER 1.8	6-phospho-beta- glucosidase (EC 3.2.1.86) bgIB - Escherichia coli	pir B65175 B65175	85%	1	540
HSIDW39	1211446	286	blastx.2	PFAM: Glycosyl hydrolases family 1	PF00232	87.26	17	289
HSIDW39	775139	823	HMNER 2.1.1	Cytosolic beta- glucosidase (Fragment).	sp CAC08178 CAC0 8178	99%	56	748
HSIDW39	775139	823	HMNER 2.1.1	PFAM: Glycosyl hydrolase family 1	PF00232	134	28	372

				blastx.2	cytosolic beta-glucosidase [Cavia porcellus]	gb AAB41058.1	84%	1	363
HSIDW39	830774	824		HMMER 2.1.1	PFAM: Glycosyl hydrolase family 1	PF00232	155.5	42	419
HPMLD30	1226192	287		blastx.2	alpha-glucosidase (EC 3.2.1.20) - Escherichia coli	pir C64769 C64769	96%	44	1543
HPMLD30	937414	825		HMMER 1.8	PFAM: Alpha amylases (family of glycosyl hydrolases)	PF00128	18.21	402	479
				blastx.2	maltodextrin glucosidase [Escherichia coli]	gb AAB40159.1	99%	30	485
HOEKP17	1204712	288		blastx.2	FLAVOHEMOPROTEIN B5+B5R	sp Q9UHI9 Q9UHI9	90% 97%	749 214	1675 870
HOEKP17	931049	826		HMMER 2.1.1	PFAM: Heme-binding domain in cytochrome b5 and oxidoreductases	PF00173	69.6	258	428
				blastx.14	(AL032654) similar to Heme-binding domain in 1	gi 3881161 emb CAA 21721.1	60% 35% 36% 60% 50% 39% 57% 55% 45%	261 1118 906 156 1253 1565 1352 1055 580	473 1285 1013 215 1318 1648 1393 1081 639
HFXDP67	1228141	289		blastx.2	hypothetical protein b0872 - Escherichia coli	pir H64825 H64825	95%	240	1205
HFXDP67	526951	827		HMMER 1.8	PFAM: FAD/NAD- binding domain in	PF00175	13.6	293	415

HJABA59	1199933	290	blastx.2	oxidoreductases	sp Q9UBK8 Q9UBK8	91%	2	904
				METHIONINE SYNTHASE REDUCTASE.				
HJABA59	713642	828	HMMER 1.8	PFAM: FAD/NAD-binding domain in oxidoreductases	PF00175	100.6	423	797
HKXIB03	1129055	291	blastx.2	CYTOCHROME B5 REDUCTASE B5R.2.	sp Q9UHH0 Q9UHH0	93% 82% 88%	197 2 70	370 88 96
HKXIB03	924636	829	HMMER 1.8	PFAM: FAD/NAD-binding domain in oxidoreductases	PF00175	31.48	192	326
			blastx.2	(AL133582) hypothetical protein [Homo sapiens]	emb CAB63726.1	85%	144	371
HKMMF49	1124742	292	blastx.2	Kidney superoxide-producing NADPH oxidase.	sp BAA95695 BAA95695	100%	10	600
HKMMF49	677960	830	HMMER 2.1.1	PFAM: Ferric reductase like transmembrane component	PF01794	63.6	79	294
HLDOG51	1151491	293	blastx.2	Neurospora crassa hypothetical protein 15E6.170 - Neurospora crassa	pir T48809 T48809	40% 32%	163 654	522 800
HLDOG51	918840	831	HMMER 2.1.1	PFAM: Oxidoreductase FAD/NAD-binding domain	PF00175	62.6	524	904
			blastx.14	phenolhydroxylase component [Acinetobacter]	gi 535285 emb CAA85385.1	32% 36%	269 860	370 967

HSVAI25	1130819	294	blastx.2	calcoaceticus]			37%	647	727
				Hypothetical 12.9 kDa protein.	sp BAB12124 BAB12124		42%	527	583
HSVAI25	577154	832	HMMER 1.8	PFAM: FAD/NAD-binding domain in oxidoreductases	PF00175		44%	215	268
							58%	524	652
							66%	663	761
HSXCP56	924635	295	HMMER 2.1.1	PFAM: FAD/NAD-binding Cytochrome reductase	PF00970		7.34	126	212
							162.3	243	500
			blastx.2	CYTOCHROME B5 REDUCTASE B5R.2.	sp Q9UHH0 Q9UHH0		91%	171	950
HBCAT08	1167275	296	blastx.2	PXN PROTEIN.	sp Q9VZZ4 Q9VZZ4		100%	142	240
							49%	71	2419
							37%	2237	2461
							50%	3295	3351
							36%	157	246
HBCAT08	920940	833	HMMER 1.8	PFAM: Peroxidases	PF00141		32.87	3	347
			blastx.14	similar to D.melanogaster peroxidase(U11052) [Homo sapiens]	gi 1504040 dbj BAA13219.1		92%	183	347
							93%	3	134
							92%	160	198
							29%	133	183
HHFBUS3	104855	297	blastx.2	subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form A - human	pir A39490 A39490		85%	4	570
HHFBUS3	837647	834	HMMER 2.1.1	PFAM: Proprotein convertase P-domain	PF01483		254.1	381	797
HTTDO45	942505	298	HMMER	PFAM: Thiolase	PF00108		794.8	459	1637

			2.1.1		3-oxoacyl-CoA thiolase - human	pir S43440 S43440	92%	456	1640
HTPII72	1104236	299	blastx.2		valine--tRNA ligase (EC 6.1.1.9) - rat (fragment)	pir PN0473 PN0473	51%	4	657
HTPII72	958035	835	HMMER 1.8		PFAM: tRNA synthetases class I	PF00133	280.02	4	645
			blastx.14		transfer RNA-Val synthetase [Rattus norvegicus]	gi 207625 gb AAA42320.1	56% 51% 58%	4 589 780	576 750 866
H6BSE22	1151371	300	blastx.2		UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (EC 3.1.2.15) 1 1 1	sp Q9Y5T5 UBPG_HUMAN	99%	156	623
H6BSE22	969019	836	HMMER 2.1.1		PFAM: Ubiquitin carboxyl-terminal hydrolases family 2	PF00442	41.8	738	833
			blastx.14		(AF126736) ubiquitin processing protease [Homo sapiens]	gi 4454565 gb AAD20949.1	94% 100% 94% 100% 42% 50%	672 156 1482 1573 1452 781	1493 602 1538 1599 1514 810
HDPAE43	1220621	301	blastx.2		Ubiquitin specific protease (Fragment).	sp AAF66953 AAF66953	80%	114	1586
HDPAE43	864998	837	HMMER 2.1.1		PFAM: Ubiquitin carboxyl-terminal hydrolases family 2	PF00442	63.9	236	331
HDPFM16	1193042	302	blastx.2		CG8830 PROTEIN.	sp Q9V6C0 Q9V6C0	53%	180	470

HDPFM16	810401	838	HMMER 2.1.1	PFAM: Ubiquitin carboxyl-terminal hydrolases family 2	PF00442	50% 30% 41% 41%	983 1571 611 1319	1201 1828 778 1435
HFPCN10	1151478	303	blastx.2	CDNA FLJ10809 FIS, CLONE NT2RP4000927, WEAKLY SIMILAR TO 11	sp BAA91825 BAA9 1825	62 69%	163 330	258 518
HFPCN10	915568	839	HMMER 1.8 blastx.14	PFAM: Ubiquitin carboxyl-terminal hydrolases family 2 (AL031525) ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe]	PF00442 gi 3560166 emb CAA 20678.1	32.31 50% 33%	417 345 466	470 464 555
HLQFO35	933901	840	HMMER 1.8	PFAM: Ubiquitin carboxyl-terminal hydrolases family 2	PF00442	11.44	131	181
HMTWTU94	1150834	305	blastx.2	UBIQUITIN CARBOXYL- TERMINAL HYDROLASE 12 (EC 3.1.2.15) 1 1 1	sp O75317 UBPC_H UMAN	92%	162	536
HMTWTU94	705880	841	HMMER 2.1.1	PFAM: Ubiquitin carboxyl-terminal hydrolases family 2	PF00442	58.8	231	326

HSATQ28	1124600	306	blastx.2	PRO0758.	sp AAF71030 AAF71030	86%	222	491
HSATQ28	866951	842	HMMER 1.8	PFAM: Ubiquitin carboxyl-terminal hydrolases family 2	PF00442	11.1	90	122
HTPIL46	1196787	307	blastx.2	Cyld protein.	sp CAB93533 CAB93533	99%	963	1859
						99%	246	962
						99%	1870	2265
						37%	669	842
						37%	1596	1754
HTPIL46	973570	843	HMMER 2.1.1	PFAM: CAP-Gly domain	PF01302	28.2	872	955
			blastx.2	(AF161542) HSPC057 [Homo sapiens]	gb AAF29029.1 AF161542_1	93%	626	2167
						100%	2143	2169
						45%	512	577
HNGEN37	1103305	308	blastx.2	indole-3-glycerol-phosphate synthase (EC 4.1.1.48) / I coli	pir A64874 GWEC	99%	1	531
HNGEN37	663955	844	HMMER 2.1.1	PFAM: Indole-3-glycerol phosphate synthases	PF00218	125.4	2	223
HLMDO77	974855	309	HMMER 1.8	PFAM: Trypsin	PF00089	114.97	116	523
			blastx.2	Complement C1r-like proteinase precursor.	sp AAF44349 AAF44349	100%	116	547
HNKAZ51	1154961	310	blastx.2	SERINE PROTEASE DESC1.	sp Q9UL52 Q9UL52	48%	100	957
HNKAZ51	947067	846	HMMER 1.8	PFAM: Trypsin	PF00089	124.58	259	594
			blastx.2	(AF064819) serine protease DESC1 [Homo	gb AAF04328.1 AF064819_1	42%	100	603
						35%	677	832

HOGDR01	919899	311	HMMER 1.8	sapiens] PFAM: Trypsin	PF00089	46%	603	686
HOGDR01	947085	847	blastx.2 HMMER 1.8	SP001LA (FRAGMENT). PFAM: Trypsin	sp O43342 O43342. PF00089	99% 320.16	165 161	890 871
HUKEP18	957456	312	blastx.2 HMMER 1.8	(AC003965) SP001LA [Homo sapiens] PFAM: Trypsin	gb AAB93671.1 PF00089	99% 82.96	155 729	967 361
HWHGF95	1155021	313	blastx.2	TESTES-SPECIFIC PROTEIN TSP50. KALLIKREIN 9 PRECURSOR (EC 3.4.21.-) (KALLIKREIN- LIKE 1	sp Q9UI38 Q9UI38 PF00089	100% 94%	735 36	340 743
HWHGF95	947019	848	HMMER 1.8 blastx.2	PFAM: Trypsin (AF135026) kallikrein- like protein 3 KLK-L3 [Homo sapiens] PFAM: Aldehyde dehydrogenase family	PF00089 gb AAD26427.2 AF1 35026_1 PF00171	309.92 93% 397.1	56 35 10	724 742 642
HEMFC61	836514	314	HMMER 2.1.1 blastx.2	RETINALDEHYDE- SPECIFIC DEHYDROGENASE TYPE 2 (EC 1.2.1.-) (RALDH(II)) (RALDH- 2).	sp O94788 DHAS_H UMAN	98%	4	642
HEOQP44	942596	315	HMMER	PFAM: Beta-lactamase	PF00144	420.7	250	1026

				2.1.1	beta-lactamase (EC 3.5.2.6) - phage phi-X174	pir S47061 S47061	95%			
				blastx.2				169		1026
HHEKZ12	878267	316		HMMER 1.8	PFAM: Beta-lactamases	PF00144	132.1	102		380
				blastx.2	beta-lactamase (EC 3.5.2.6) - phage phi-X174	pir S47061 S47061	98%	21		377
							65%	377		436
HHELA35	878217	317		HMMER 2.1.1	PFAM: Beta-lactamase	PF00144	175.4	118		450
				blastx.2	beta-lactamase (EC 3.5.2.6) - phage phi-X174	pir S47061 S47061	98%	37		450
HSYBQ34	972295	849		HMMER 1.8	PFAM: Beta-lactamases	PF00144	387.58	2697		3473
HFCBA44	948533	319		HMMER 1.8	PFAM: Carboxylesterases	PF00135	34.24	315		485
				blastx.2	thiolesterase B (EC 3.-.-.-) precursor - mallard	pir A47162 A47162	56%	2		208
							60%	423		482
							48%	184		264
HOUBE50	948519	320		HMMER 1.8	PFAM: Carboxylesterases	PF00135	55.97	16		243
				blastx.2	Neurologin 3 isoform HNL3s (Fragment).	sp AAF71231 AAF71231	70%	31		243
HDPAS16	734057	321		HMMER 2.1.1	PFAM: Carbamoyl-phosphate synthase (CPSase)	PF00289	137.8	220		495
				blastx.2	3-methylcrotonyl-CoA carboxylase biotin-containing 1	sp BAA99407 BAA99407	89%	112		495
HFLAA23	960332	322		HMMER 2.1.1	PFAM: FGYY family of carbohydrate kinases	PF00370	314	137		784

HCFMZ90	922112	323	blastx.2 HMMER 1.8	L-xylulokinase (EC 2.7.1.53) - Escherichia coli PFAM: Beta-ketoacyl synthases	pir S47801 S47801	86%	8	784
			blastx.2	CDNA FLJ20604 FIS, CLONE KAT06449.	sp BAA91286 BAA9 1286	92% 98% 59%	255 67 5	866 300 100
HFCES27	1103330	324	blastx.2	CDNA FLJ20604 FIS, CLONE KAT06449.	sp BAA91286 BAA9 1286	94% 86%	506 198	1120 491
HFCES27	922115	850	HMMER 2.1.1	PFAM: Beta-ketoacyl synthase	PF00109	206.2	372	1001
			blastx.14	(AE000752) 3-oxoacyl- [acyl-carrier-protein] synthase II [Aquifex aerophilus]	gi 2984031 gb AAC0 7574.1	53% 78% 75% 37%	393 195 939 250	920 251 986 297
HSDFK78	1155464	325	blastx.2	biotin sulfoxide reductase (EC 1.-.-) 2 - Escherichia coli	pir H64949 H64949	89%	1	306
HSDFK78	582754	851	HMMER 2.1.1	PFAM: Prokaryotic molybdopterin oxidoreductases	PF00384	34.8	297	374
HSDJX58	891067	326	HMMER 1.8	PFAM: NADH- Ubiquinone/plastoquinone , various chains	PF00361	97.09	1128	1487
			blastx.2	hypothetical protein b2484 - Escherichia coli (strain K-12)	pir C65024 C65024	82%	735	1487
HSDJX58	956591	852	HMMER 1.8	PFAM: NADH- Ubiquinone/plastoquinone	PF00361	100.08	387	19

					blastx.2	, various chains						
HSLHV27	1105339	327			blastx.2	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 [Escherichia coli]	dbj BAA16372.1	100%	814	1572		
					blastx.2	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain L - Escherichia coli	pir D64999 D64999	93%	94	927		
HSLHV27	964075	853			HMMER 2.1.1	PFAM: NADH-Ubiquinone/plastoquinone (complex I), various chains	PF00361	115.1	917	615		
					blastx.2	NADH dehydrogenase I, subunit nuoL [Escherichia coli]	emb CAA48371.1	99%	91	954		
HNGFU12	1128272	328			blastx.2	REVERSE TRANSCRIPTASE (476 AA) (FRAGMENT).	sp Q85732 Q85732	55%	109	543		
HNGFU12	971170	854			HMMER 1.8	PFAM: RNase H	PF00075	55.68	102	290		
					blastx.14	reverse transcriptase (476 AA) [Woolly monkey sarcoma virus]	gi 930259 emb CAA33367.1	44% 60%	96 1	422 75		
HWLKA89	1105515	329			blastx.2	POL PROTEIN.	sp Q9WIK9 Q9WIK9	51% 54% 55% 64%	560 885 135 448	186 577 1 398		
HWLKA89	735158	855			HMMER 1.8	PFAM: RNase H	PF00075	47.76	25	165		
HLWBU48	1162653	330			blastx.2	ENDOGENOUS	sp Q15803 Q15803	84%	739	984		

HLWBU48	721520	856	HMMER 1.8	RETROVIRUS HERV- K(HML6) PROVIRAL CLONE HML6.17.1.1	PF00077	77%	672	752
HWWEY71	1204720	331	blastx.2	PFAM: Retroviral aspartyl proteases	sp P34897 GLYM_H_UMAN	64.25	14	280
				SERINE HYDROXYMETHYLTR ANSFERASE, MITOCHONDRIAL PRECURSOR 1.1		97% 97%	595 113	1623 619
HWWEY71	970546	857	HMMER 2.1.1	PFAM: Serine hydroxymethyltransferase	PF00464	423.3	257	763
			blastx.14	SERINE HYDROXYMETHYLTR ANSFERASE, MITOCHONDRIAL PRECURSOR 1 (SHMT).	sp P34897 GLYM_H_UMAN	90%	113	859
HHFGD45	1151161	332	blastx.2	superoxide dismutase (EC 1.15.1.1) (Mn) sodA [validated] - Escherichia coli	pir A24141 DSECN	100%	880	290
HHFGD45	584855	858	HMMER 1.8	PFAM: Iron/manganese superoxide dismutases (SODM)	PF00081	111.46	133	267
HNHEB44	1161293	333	blastx.2	superoxide dismutase (EC 1.15.1.1) (Mn) sodA [validated] - Escherichia coli	pir A24141 DSECN	100%	23	613
HNHEB44	683284	859	HMMER 1.8	PFAM: Iron/manganese superoxide dismutases	PF00081	100.87	31	150

HMACX92	1151497	334	blastx.2	(SODM) L-serine dehydratase (EC 4.2.1.13) - rat	pir S01009 DWR TT	50%	176	1132
HMACX92	922250	860	HMMER 2.1.1	PFAM: Pyridoxal-phosphate dependent enzyme	PF00291	224.5	203	1105
			blastx.2	serine dehydratase (AA 1 - 327) [Rattus norvegicus]	emb CAA68721.1	61%	197	1153
HNTBW57	1193070	335	blastx.2	CDNA FLJ10916 FIS, CLONE OVARC100309, WEAKLY SIMILAR TO 1	sp BAA91904 BAA91904	80% 100%	958 613	1302 777
HNTBW57	867327	861	HMMER 1.8	PFAM: Serine/threonine dehydratases, cysteine synthase and cystathionine	PF00291	41.43	425	673
HBSDC13	1105677	336	blastx.2	tartronate-semialdehyde synthase (EC 4.1.1.47) - Escherichia coli	pir JT0742 JT0742	68% 83% 51% 85% 96%	353 124 622 840 47	718 423 990 959 130
HBSDC13	657402	862	HMMER 1.8	PFAM: Thiamine pyrophosphate enzymes	PF00205	26.75	3	182
HCWBX21	920486	337	HMMER 1.8	PFAM: Thiamine pyrophosphate enzymes	PF00205	22.15	82	261
			blastx.2	tartronate-semialdehyde synthase (EC 4.1.1.47) - Escherichia coli	pir JT0742 JT0742	88% 96% 43%	85 8 374	369 91 442
HFRBW72	916944	338	HMMER 2.1.1	PFAM: Thiamine pyrophosphate enzymes	PF00205	92.9	443	664

HSLJX23	1105530	339	blastx.2	pyruvate dehydrogenase (cytochrome) (EC 1.2.2.2) - Escherichia coli	pir A23648 DEECPC	81%	407	676
HSLJX23	837470	863	blastx.2	tartronate-semialdehyde synthase (EC 4.1.1.47) - Escherichia coli	pir JT0742 JT0742	98%	2	496
HSLJX90	1105297	340	HMMER 1.8	PFAM: Thiamine pyrophosphate enzymes	PF00205	57.57	2	193
HSLJX90	787575	864	blastx.2	pyruvate dehydrogenase (cytochrome) (EC 1.2.2.2) - Escherichia coli	pir A23648 DEECPC	100%	1	438
HAUAI67	1102604	341	HMMER 2.1.1	PFAM: Thiamine pyrophosphate enzymes	PF00205	95.2	2	274
HAUAI67	929241	865	blastx.2	HSPC150.	sp AAF29114 AAF29 114	100%	137	727
HDPTA89	953718	342	HMMER 1.8	PFAM: Ubiquitin- conjugating enzymes	PF00179	128.71	236	508
HMCBN45	927125	343	blastx.14	ubiquitin-conjugating enzyme [Schizosaccharomyces pombe]	gi 2330662 emb CAB 11183.1	54% 67% 32%	344 242 132	514 334 224
HTTJY18	1223495	344	HMMER 1.8	PFAM: Ubiquitin- conjugating enzymes	PF00179	74.19	173	424
			blastx.2	UBC6P HOMOLOG.	sp Q9QX58 Q9QX58	95%	173	430
			HMMER 1.8	PFAM: Ubiquitin- conjugating enzymes	PF00179	115.78	234	677
			blastx.2	hypothetical protein R09B3.4 - Caenorhabditis elegans	pir T24069 T24069	53%	216	680
			blastx.2	Non-Canonical Ubiquitin	sp CAB83212 CAB8	83%	376	1281

HTTY18	950989	866	HMMER 1.8 blastx.2	Conjugating Enzyme 1 (NCUBE1). PFAM: Ubiquitin- conjugating enzymes (AF151834) CGI-76 protein [Homo sapiens]	3212	100%	330	365
HMAJL09	1157337	345	blastx.2	hypothetical 29.7K protein, ibpA-gyrB intergenic region - Escherichia coli (strain K- 12)	gb AAD34071.1 AF1 51834.1 pir B65172 QQECGB	99% 98%	292 269	1263 526
HMAJL09	950168	867	HMMER 1.8 blastx.14	PFAM: ADP-glucose pyrophosphorylase f270 [Escherichia coli]	PF00483	150.92	20	256
HSVCH37	558195	346	HMMER 2.1.1	PFAM: 3'5'-cyclic nucleotide phosphodiesterase	gi 290545 gb AAA62 048.1 PF00233	100% 100% 30	254 468 18	469 512 98
HTOCG37	708888	347	HMMER 2.1.1 blastx.2	PFAM: 3'5'-cyclic nucleotide phosphodiesterase 3'5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 8B, 1	PF00233 pir JE0293 JE0293	65.1 100% 53%	42 6 179	215 203 340
HBXAW47	771624	348	HMMER 2.1.1 blastx.2	PFAM: Protein phosphatase 2C PROTEIN PHOSPHATASE 2C..	PF00481 sp Q9Z1Z6 Q9Z1Z6	80.5 85%	273 270	560 578
HBXAW27	909801	349	HMMER 2.1.1	PFAM: Phosphatidylinositol-	PF00388	113.6	1642	1797

				specific phospholipase C, X domain					
HSLJE54	926924	350	blastx.2	Phospholipase C-beta-1a.	sp CAB98142 CAB98142	97%	1243	1803	
			HMMER 2.1.1	PFAM: Pyridoxal-dependent decarboxylase conserved domain	PF00282	35.8	342	536	
			blastx.2	CYSTEINE SULFINIC ACID DECARBOXYLASE-RELATED PROTEIN 4.	sp Q9UNJ5 Q9UNJ5	98% 92% 85% 100%	198 542 721 885	548 739 885 908	
HBXBG65	932780	351	HMMER 1.8	PFAM: Cytochrome P450	PF00067	46.55	2	535	
			blastx.2	CHOLESTEROL 24-HYDROXYLASE.	sp Q9Y6A2 Q9Y6A2	98%	2	535	
HE8CG83	933609	352	HMMER 2.1.1	PFAM: Protein phosphatase 2C	PF00481	42.6	757	942	
			blastx.2	SCOP.	sp Q9WTR8 Q9WTR8	90% 70% 70% 60% 43% 30% 36%	321 712 1 977 41 118 369	707 1110 348 1021 151 279 443	
HOGCW55	953161	353	HMMER 2.1.1	PFAM: Aminotransferases class-V	PF00266	56.5	132	341	
			blastx.2	probable phosphoserine transaminase (EC 2.6.1.52), progesterone-	pir A26998 A26998	85% 77%	132 355	356 381	

HNTND64	954871	354	HMMER 2.1.1 blastx.2	induced, endometrial - rabbit PFAM: Cytochrome P450	PF00067	28.2	10	225
				cytochrome P450 - golden hamster	pir I48164 I48164	37% 47%	10 261	264 329
HHAWC08	957942	355	HMMER 1.8 blastx.2	PFAM: IMP dehydrogenase / GMP reductase	PF00478	231.99	361	978
				Guanosine monophosphate reductase isolog.	sp BAA93080 BAA9 3080	100% 100%	334 975	975 1376
HPFEN04	964824	356	HMMER 1.8 blastx.2	PFAM: Aminotransferases class- III pyridoxal-phosphate	PF00202	33.54	259	489
				CG8745 PROTEIN.	sp Q9VU95 Q9VU95	62%	148	492
HTZMB51	496523	357	HMMER 2.1.1 blastx.2	PFAM: Lyase adenylosuccinate lyase (EC 4.3.2.2) - Escherichia coli	PF00206	112.9	61	399
					pir S19212 S19212	97% 71%	73 2	399 127
HNHDK43	529500	358	HMMER 1.8 blastx.2	PFAM: tRNA synthetases class II lysine--tRNA ligase (EC 6.1.1.6) - Escherichia coli	PF00152	55.51	208	372
					pir B65073 SYECKT	85% 90%	58 368	372 397
HTTDP32	558751	359	HMMER 2.1.1 blastx.2	PFAM: tRNA synthetases class I (L, M and V) PROBABLE LEUCYL- TRNA SYNTHETASE, MITOCHONDRIAL	PF00133	76	7	261
					sp Q15031 SYLM_H UMAN	98% 84% 45%	1 267 320	261 365 424

HSLEP27	572920	360	HMMER 2.1.1 blastx.2	PRECURSORS 1 PFAM: tRNA synthetases class I (I, L, M and V) leucine--tRNA ligase (EC 6.1.1.4) [validated] - Escherichia coli	PF00133 pir H64798 SYECL	133.5 96% 96%	5 14 405	409 599
HMTAL73	621705	361	HMMER 2.1.1 blastx.2	PFAM: Isocitrate and isopropylmalate dehydrogenases isocitrate dehydrogenase (NAD+) (EC 1.1.1.41) beta chain isoform B - human	PF00180 pir T13147 T13147	94.5 75% 100%	241 103 2	423 450 100
HMHQBQ53	715301	362	HMMER 2.1.1 blastx.2	PFAM: Nucleotidyl transferase GDP-MANNOSE PYROPHOSPHORYLAS E A.	PF00483 sp Q9Y5P5 Q9Y5P5	45.8 100% 100%	237 231 376	368 377 423
HBICG44	715860	363	HMMER 2.1.1 blastx.2	PFAM: Thiolase 3-oxoacyl-CoA thiolase - human	PF00108 pir S43440 S43440	33.1 100%	189 189	272 272
HSKXN70	753717	364	HMMER 2.1.1 blastx.2	PFAM: TPR Domain CG5038 PROTEIN. PFAM: Histidine acid phosphatase acid phosphatase (EC 3.1.3.2) precursor - Escherichia coli	PF00515 sp Q9VVF81 Q9VVF81 PF00328 pir B36733 B36733	31.4 40% 118.4 77% 92%	267 114 75 3 341	347 344 338 518 463

HHFFP57	835955	366	HMMER 2.1.1	PFAM: Signal peptidase I	PF00461	32.1	218	514
HFKJW01	836491	367	blastx.2	CG11110 PROTEIN.	sp Q9V959 Q9V959	57%	140	574
			HMMER 2.1.1	PFAM: Aldehyde dehydrogenase family	PF00171	174	96	440
			blastx.2	lactaldehyde dehydrogenase (EC 1.2.1.22) aldA - Escherichia coli	pir A38165 A38165	100%	96	440
HSDFL63	836498	368	HMMER 2.1.1	PFAM: Aldehyde dehydrogenase family	PF00171	127.4	1	234
			blastx.2	RETINALDEHYDE- SPECIFIC DEHYDROGENASE TYPE 2 (EC 1.2.1.-) (RALDH(II)) (RALDH- 2).	sp O94788 DHAS_H UMAN	100%	1	249
HLD0008	857070	369	HMMER 2.1.1	PFAM: Ubiquitin carboxyl-terminal hydrolase family 2	PF00443	32.4	36	137
			blastx.2	CDNA FLJ10785 FIS, CLONE NT2RP4000457, WEAKLY SIMILAR TO 1	sp BAA91807 BAA9 1807	100% 80%	3 403	401 570
HMSHN43	867363	370	HMMER 2.1.1	PFAM: Nucleotidyl transferase	PF00483	53.7	70	231
			blastx.2	GDP-MANNOSE PYROPHOSPHORYLAS E A.	sp Q9Y5P5 Q9Y5P5	90%	64	342
HBXCT92	871044	371	HMMER	PFAM: Nucleotidyl	PF00483	49.7	105	473

			2.1.1	transferase				
			blastx.2	Eukaryotic translation initiation factor EIF2B subunit 3.	sp AAF91351 AAF91351	97%	96	1451
H6EDP44	875744	372	HMMER 2.1.1	PFAM: Nucleotidyl transferase	PF00483	129.6	190	768
			blastx.2	GDP-MANNOSE PYROPHOSPHORYLAS E B.	sp Q9Y5P6 Q9Y5P6	99% 100% 100% 32%	199 804 65 837	801 968 187 938
HLJBF94	875745	373	HMMER 2.1.1	PFAM: Nucleotidyl transferase	PF00483	89.2	261	539
			blastx.2	GDP-MANNOSE PYROPHOSPHORYLAS E B.	sp Q9Y5P6 Q9Y5P6	81%	258	668
HTEHO28	877182	374	HMMER 1.8	PFAM: Pyridine nucleotide-disulphide oxidoreductases class-I	PF00070	206.97	1166	441
			blastx.2	Thioredoxin reductase TR2 (Fragment).	sp AAD51325 AAD51325	97% 85% 97% 41%	1226 1857 2123 1383	432 1147 1869 1315
HE9PC30	880696	375	HMMER 1.8	PFAM: Ubiquitin-conjugating enzymes	PF00179	69.1	85	285
			blastx.2	CGI-76 PROTEIN.	sp Q9Y385 Q9Y385	98% 96% 60%	43 555 527	381 638 586
HLMDN29	881288	376	HMMER 2.1.1	PFAM: Ubiquitin carboxyl-terminal hydrolase family 2	PF00443	34.2	315	506

HWBCF78	911355	377	blastx.2	CG8830 PROTEIN.	sp Q9V6C0 Q9V6C0	43%	9	218
						31%	399	503
HUKEN49	911465	378	HMMER 2.1.1	PFAM: Myosin head (motor domain)	PF00063	31.2	202	285
			blastx.2	myosin-I α - mouse	pir A59300 A59300	89%	148	288
			HMMER 1.8	PFAM: Myosin head (motor domain) (contains ATP/GTP binding P-loop)	PF00063	53.97	125	274
			blastx.2	Myosin V.	sp AAF78910 AAF78910	66%	3	128
HCUDS02	914401	379	HMMER 2.1.1	PFAM: Nucleotidyl transferase	PF00483	54%	125	274
			blastx.2	CDNA FLJ10137 FIS, CLONE HEMBA1003136, WEAKLY SIMILAR TO 1	sp BAA91460 BAA91460	40%	333	431
HTTJU40	914402	380	HMMER 2.1.1	PFAM: Nucleotidyl transferase	PF00483	91.6	84	650
			blastx.2	GDP-MANNOSE PYROPHOSPHORYLAS E A.	sp Q9Y5P5 Q9Y5P5	98%	78	782
HFXJX41	915649	381	HMMER 2.1.1	PFAM: Phosphoglucomutase/phosphomannomutase	PF00408	99%	907	1335
			blastx.2	hypothetical protein b0644 - Escherichia coli	pir B64799 B64799	64%	755	1006
			HMMER 2.1.1	Phosphoglucomutase/phosphomannomutase	PF00408	23.8	43	372
			blastx.2	hypothetical protein b0644 - Escherichia coli	pir B64799 B64799	100%	40	417
			HMMER 2.1.1	Phosphoglucomutase/phosphomannomutase	PF00408	100%	440	496
			blastx.2	hypothetical protein b0644 - Escherichia coli	pir B64799 B64799	36.5	491	682
			HMMER 2.1.1	Phosphoglucomutase/phosphomannomutase	PF00408	100%	3	308
			blastx.2	hypothetical protein b0644 - Escherichia coli	pir B64799 B64799	100%	308	496
			HMMER 2.1.1	Phosphoglucomutase/phosphomannomutase	PF00408	45%	6	308
			blastx.2	hypothetical protein b0644 - Escherichia coli	pir B64799 B64799	43%	3	308

HSLCK91	915650	382	HMMER	PFAM:	PF00408		36%	6	308
			2.1.1	Phosphoglucosyltransferase/phosphomannomutase			39%	3	308
			blastx.2	phosphoglucosyltransferase (EC 5.4.2.2) - Escherichia coli			35%	212	553
							37%	3	281
							35%	30	305
HSLAO29	917349	383	HMMER	PFAM: Serine	PF00464	pir G64803 G64803	39%	308	496
			2.1.1	hydroxymethyltransferase			33%	308	496
			blastx.2	SERINE			84%	1	375
				HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL			43	363	431
				PRECUSOR 1 1			92%	137	373
HRDBJ38	917583	384	HMMER	PFAM: Trypsin	PF00089	sp P34897 GLYM_HUMAN	52%	363	536
			2.1.1				48%	427	534
			blastx.2	SERINE PROTEASE (FRAGMENT)			62%	23	856
				PFAM: Aldehyde dehydrogenase family			138.5	3	278
				lactaldehyde dehydrogenase (EC 1.2.1.22) aldA - Escherichia coli			98%	3	275

HWLHU02	918520	386	HMMER 2.1.1	PFAM: Hexokinase	PF00349	286.7	3	395
			blastx.2	Hexokinase II.	sp CAA86476 CAA86476	79% 66%	3 3	395 395
HEAHA84	919363	387	HMMER 2.1.1	PFAM: Myosin head (motor domain)	PF00063	36.3	87	245
			blastx.2	myosin I myr 4 - rat	pir A53933 A53933	96% 100%	87 794	794 1216
HBMXQ90	922114	388	HMMER 2.1.1	PFAM: Beta-ketoacyl synthase	PF00109	20.5	218	301
			blastx.2	CDNA FLJ20604 FIS, CLONE KAT06449.	sp BAA91286 BAA91286	66% 96%	301 215	462 301
HOEJV72	930778	389	HMMER 1.8	PFAM: Nucleoside diphosphate kinases	PF00334	103.55	362	757
			blastx.2	NM23-H7.	sp Q9Y5B8 Q9Y5B8	95% 29%	89 368	847 754
HRDBH58	933364	390	HMMER 1.8	PFAM: Aldehyde dehydrogenases	PF00171	175.49	536	1558
			blastx.2	probable aldehyde dehydrogenase PA4073 [imported] - Pseudomonas aeruginosa (strain PAO1)	pir H83136 H83136	29% 34%	569 244	1528 450
HCE3E13	951413	391	HMMER 2.1.1	PFAM: tRNA synthetases class I (L, M and V)	PF00133	95.6	148	603
			blastx.2	valine-tRNA ligase precursor, mitochondrial - fission yeast (Schizosaccharomyces pombe)	pir T39630 T39630	40% 41% 44% 83%	151 4 569 645	603 213 649 662
HUKFO68	951652	392	HMMER	PFAM: Hexokinase	PF00349	173.1	83	340

			2.1.1	Hexokinase I (Fragment).	sp AAAF28854 AAAF28854	76%	83	355
			blastx.2			47%	83	373
						80%	3	80
						36%	3	77
HFXJW08	959204	393	HMMER 2.1.1	PFAM: tRNA synthetases class I (L, M and V)	PF00133	86.6	224	487
			blastx.2	leucine--tRNA ligase (EC 6.1.1.4) [validated] - Escherichia coli	pir H64798 SYBCL	82%	224	676
						100%	3	230
HBTAD04	407351	394	blastx.2	malate synthase (EC 4.1.3.2) A - Escherichia coli	pir A32649 SYECMA	98%	240	1
HBTAD04	422687	868	HMMER 2.1.1	PFAM: Acetyltransferase (GNAT) family	PF00583	36.5	427	161
HE8FG51	465267	395	HMMER 2.1.1	PFAM: Eukaryotic initiation factor 5A hypusine (eIF-5A)	PF01287	165.7	4	258
			blastx.2	EIF-5A2.	sp AAAF98810 AAAF98810	98%	7	267
HTPDU31	503077	396	HMMER 2.1.1	PFAM: haloacid dehalogenase-like hydrolase	PF00702	26.3	147	296
			blastx.2	DJ37E16.5 (NOVEL PROTEIN SIMILAR TO NITROPHENYLPHOSPHATASES 1	sp Q9UGY2 Q9UGY2	94%	54	323
						100%	25	72
						100%	323	364
HMUBV12	549423	397	HMMER 2.1.1	PFAM: Hyaluronidase	PF01630	50.7	196	303
HM(HBS90	574062	398	HMMER	PFAM: UBA domain	PF00627	35.6	436	543

				2.1.1						
			blastx.2	HRIHFB2157-LIKE PROTEIN (FRAGMENT).	sp Q9UHX4 Q9UHX4	61% 100%	58 3	561 59		
HLHG34	575733	399	HMMER 1.8 blastx.2	PFAM: C-5 cytosine- specific DNA methylases PUTATIVE DNA CYTOSINE METHYLTRANSFERAS E DNMT2.	PF00145 sp O43669 O43669	33.72 100%	284 2	436 436		
HELHC55	577384	400	HMMER 2.1.1 blastx.2	PFAM: Copper amine oxidase amine oxidase (copper- containing) (EC 1.4.3.6) tynA precursor - Escherichia coli	PF01179 pir E64889 E64889	88.8 96%	39 3	173 173		
HKAAZ66	592105	401	HMMER 2.1.1 blastx.2	PFAM: Calpain family cysteine protease Calpain large polypeptide L2.	PF00648 sp AAF99682 AAF99682	164.9 99% 98% 87%	222 90 416 648	422 422 640 671		
HHSCN33	657367	402	HMMER 2.1.1 blastx.2	PFAM: HECT-domain (ubiquitin-transferase). NEDD4-like ubiquitin ligase 1.	PF00632 sp BAB13352 BAB13352	58.3 91%	166 1	348 390		
HNGJQ15	660310	403	HMMER 2.1.1 blastx.2	PFAM: Histone deacetylase family CDNA FLJ10170 FIS, CLONE HEMBA1003690,	PF00850 sp BAA91474 BAA91474	33.2 75% 47%	70 70 196	192 192 264		

HDJME16	661396	404	HMMER 2.1.1 blastx.2	WEAKLY SIMILAR TO 1 PFAM: FF domain	PF01846	53.7	34	183
HNTNR64	670033	405	HMMER 2.1.1 blastx.2	HUNTINGTON YEAST PARTNER C. PFAM: Kelch motif	sp Q9WVC9 Q9WV C9 PF01344	84%	1	486
HMICO24	677036	406	HMMER 2.1.1 blastx.2	CDNA FLJ11078 FIS, CLONE PLACE1005102, WEAKLY SIMILAR TO 1 PFAM: Kelch motif	sp BAA91990 BAA9 1990 PF01344	36% 34% 47% 43% 89.1	30 54 347 350 25	344 314 448 445 147
HSIAC23	679292	407	HMMER 2.1.1 blastx.2	LYMPHOCYTE ACTIVATION- ASSOCIATED PROTEIN. PFAM: Chlorohydrolase	sp Q9Y2X2 Q9Y2X2 PF01685	92% 49% 55% 44% 52% 80% 100% 100% 47% 25.7	25 25 55 25 85 285 242 2 236 194	261 243 231 243 234 344 283 22 286 358
HSLFL74	685897	408	HMMER 2.1.1	GUANINE DEAMINASE (EC 3.5.4.3) (GUANASE) (GUANINE 1) PFAM: RNB-like proteins	sp Q9R111 GUAD_ MOUSE PF00773	62% 87% 243.4	62 10 21	457 108 425

			blastx.2	exoribonuclease II (EC 3.1.13.1) - Escherichia coli	pir A64877 A64877	78%	705	1346
						97%	3	428
						75%	434	892
						94%	877	933
						48%	990	1064
HSDJD53	698259	409	HMMER 2.1.1	PFAM: Nitroreductase family	PF00881	86.9	193	513
			blastx.2	hypothetical protein, 20K (selD-sppA intergenic region) - Escherichia coli	pir A40360 A40360	80%	190	624
HCEBF33	702955	410	HMMER 2.1.1	PFAM: HECT-domain (ubiquitin-transferase).	PF00632	248.4	15	581
			blastx.2	Ubiquitin-protein ligase 1.	sp AAF36454 AAF36454	51%	21	581
HAPQW27	705518	411	HMMER 2.1.1	PFAM: Sterol O-acyltransferase	PF01800	180.1	1	279
			blastx.2	AGRP1 PROTEIN.	sp O75907 O75907	62%	1	432
HCFLZ28	707183	412	HMMER 2.1.1	PFAM: ThiF family	PF00899	93.7	166	444
			blastx.2	SUMO-1-ACTIVATING ENZYME E1 N SUBUNIT.	sp O95717 O95717	95% 83%	142 495	447 545
HWCAB58	710377	413	HMMER 2.1.1	PFAM: Kelch motif	PF01344	53.3	21	164
			blastx.2	Kelch related protein 1.	sp CAC08185 CAC08185	49% 59% 29% 28%	3 302 3 18	275 448 266 245
HLMCMC57	713770	414	HMMER 2.1.1	PFAM: Acetyltransferase (GNAT) family	PF00583	31	272	406

			blastx.2	diamine N-acetyltransferase (EC 2.3.1.57) - spiny mouse (Mus saxicola)	pir S43430 S43430	39% 55%	272 55	478 135
HMELH37	717556	415	HMMER 2.1.1	PFAM: Initiation factor 2 subunit family	PF01008	101.1	163	432
			blastx.2	probable translation initiation factor eIF-2B delta chain - human (fragment)	pir T08757 T08757	95% 96%	163 3	441 164
HNGJ55	722240	416	HMMER 2.1.1	PFAM: MaoC like domain	PF01575	117.2	16	285
			blastx.2	membrane protein maoC - Escherichia coli	pir F64889 F64889	100%	1	282
HNGJ55	868063	869	HMMER 2.1.1	PFAM: MaoC like domain	PF01575	117.2	308	577
HHGDG42	724795	417	HMMER 2.1.1	PFAM: Acetyltransferase (GNAT) family	PF00583	24.9	179	313
			blastx.2	diamine N-acetyltransferase (EC 2.3.1.57) - spiny mouse (Mus saxicola)	pir S43430 S43430	40%	179	349
HMTMF31	731302	418	HMMER 2.1.1	PFAM: ThiF family	PF00899	88	50	415
			blastx.2	CG1749 PROTEIN.	sp Q9VYY3 Q9VYY3	72%	62	424
HSDIF59	739212	419	HMMER 2.1.1	PFAM: Flavin reductase like domain	PF01613	139.4	411	683
			blastx.2	4-HYDROXYPHENYLAC	sp P75893 P75893	90%	294	740

HNDAG60	751953	420	ETATE 3-MONOOXYGENASE (EC 1.14.13.3).	PFAM: Kelch motif	PF01344	53.8	177	320
			HMMER 2.1.1	blastx.2	sp Q9Y480 Q9Y480	67% 75% 100% 36% 32% 34% 28% 30% 33%	174 296 3 174 174 174 323 174 320	425 445 80 323 320 320 436 320 418
HSLDS79	753247	421	PFAM: Trehalase		PF01204	1028.4	117	1622
			HMMER 2.1.1	blastx.2	pir S04782 S04782	100%	102	1622
			alpha, alpha-trehalase (EC 3.2.1.28) precursor, periplasmic - Escherichia coli					
HSLDS79	879215	870	PFAM: Trehalase		PF01204	102.4	132	392
HFBCQ61	769102	422	PFAM: Kelch motif		PF01344	83.8	117	245
			HMMER 2.1.1	blastx.2	pir T33222 T33222	53% 41% 42% 37%	3 3 12 9	245 242 245 245
			hypothetical protein W02G9.2 - Caenorhabditis elegans					
HRACD17	769103	423	PFAM: Kelch motif		PF01344	108.4	245	343
			HMMER 2.1.1					

			blastx.2	CDNA FLJ10836 FIS, CLONE NT2RP4001228, WEAKLY SIMILAR TO 1	sp BAA91845 BAA91845	94%	2	358
						43%	2	325
						41%	2	337
						45%	83	343
						40%	2	355
						53%	309	386
HLDQV23	788957	424	HMMER 2.1.1	PFAM: Glycosyl transferases	PF00535	59.7	71	364
			blastx.2	hypothetical protein F13G3.6 - Caenorhabditis elegans	pir T20856 T20856	42%	68	376
HPHAF45	812327	425	HMMER 2.1.1	PFAM: Kelch motif	PF01344	88.4	22	162
			blastx.2	CDNA FLJ10262 FIS, CLONE HEMBB1000985, WEAKLY SIMILAR TO 1	sp BAA91514 BAA91514	100%	118	384
HSUME31	812373	426	HMMER 2.1.1	PFAM: Exonuclease	PF00929	118.4	4	441
			blastx.2	ISG20 PROTEIN.	sp O00441 O00441	57%	1	441
HUSHB56	815819	427	HMMER 2.1.1	PFAM: Calpain family cysteine protease	PF00648	70.1	101	346
			blastx.2	CALPAIN-LIKE PROTEASE.	sp Q9WVF0 Q9WVF0	87%	65	352
HTGDN81	824708	428	HMMER 2.1.1	PFAM: RNB-like proteins	PF00773	395.6	417	1028
			blastx.2	virulence-associated protein vacB homolog - Escherichia coli	pir S56404 S56404	97%	417	998
						94%	1	435

HSKHY26	836598	429	HMMER 2.1.1 blastx.2	PFAM: Glycosyl transferases UDP- GALNAC:POLYPEPTID E.N. ACETYL GALACTOSA MINYLTRANSFERASE.	PF00535 sp Q9UIV5 Q9UIV5	66.5	35	427
HKACD80	837698	430	HMMER 2.1.1 blastx.2	PFAM: Glycosyl hydrolase family 47 CDNA FLJ10783 FIS, CLONE NT2RP4000417, WEAKLY SIMILAR TO 1	PF01532 sp BAA91806 BAA9 1806	125.1	198	521
HHFDK48	837782	431	HMMER 2.1.1 blastx.2	PFAM: Sulfatase N-acetylgalactosamine-4- sulfatase (EC 3.1.6.12) precursor - cat	PF00884 pir A44475 A44475	143.6	13	351
HE9SS77	838043	432	HMMER 2.1.1 blastx.2	PFAM: Sulfatase CG6725 PROTEIN.	PF00884 sp Q9VEX0 Q9VEX0	112.1	213	671
HAPOK49	848205	433	HMMER 2.1.1 blastx.2	PFAM: UBA domain BS4 PROTEIN (NY- REN-18 ANTIGEN).	PF00627 sp Q9Y5A7 BS4_HU MAN	61% 78.1	3 687	671 806
HPMGN48	848318	434	HMMER 2.1.1 blastx.2	PFAM: Initiation factor 2 subunit family CG11334 PROTEIN.	PF01008 sp Q9V9X4 Q9V9X4	77% 71% 89% 264.5	195 833 47 75	872 1063 187 572
						60%	78	605

HUVHP54	849278	435	HMMER 2.1.1 blastx.2	PFAM: Dienelactone hydrolase family Hypothetical 34.2 kDa protein.	PF01738 sp AAG12612 AAG1 2612	80.3	354	1001
HSLDK59	853385	436	HMMER 2.1.1 blastx.2	PFAM: N- acetylmuramoyl-L-alanine amidase hypothetical protein b0867 precursor - Escherichia coli	PF01510 pir C64825 C64825	80.6 100% 78%	500 500 183	736 1009 557
HMWDI41	854051	437	HMMER 2.1.1 blastx.2	PFAM: Keich motif CDNA FLJ20059 FIS, CLONE COL01349.	PF01344 sp BAA90921 BAA9 0921	91.2 92%	488 2	595 592
HFVHU73	856165	438	HMMER 2.1.1 blastx.2	PFAM: RNB-like proteins ribonuclease II RNB family protein - fission yeast (Schizosaccharomyces pombe)	PF00773 pir T38518 T38518	62.5 45% 38%	6 9 253	281 281 360
HMUBJ80	858497	439	HMMER 2.1.1 blastx.2	PFAM: Histone deacetylase family CDNA FLJ10328 FIS, CLONE NT2RM2000588, WEAKLY SIMILAR TO 1	PF00850 sp BAA91545 BAA9 1545	44.9 93% 88%	233 209 477	430 490 602
HE9ML74	859297	440	HMMER 2.1.1 blastx.2	PFAM: HECT-domain (ubiquitin-transferase). CG5604 PROTEIN.	PF00632 sp Q9VL06 Q9VL06	74.3 82%	705 940	914 1269

HLQAJ01	864092	441	HMMER 2.1.1 blastx.2	PFAM: Histone deacetylase family	PF00850	40% 43%	456 3	932 350
HSLDP32	866241	442	HMMER 2.1.1 blastx.2	Class I histone deacetylase.	sp AAAF73076 AAAF73 076	100%	7	240
HPMEG40	866272	443	HMMER 2.1.1 blastx.2	PFAM: Fumarylacetoacetate (FAA) hydrolase family conserved hypothetical protein PA0318 [imported] - Pseudomonas aeruginosa (strain PAO1)	PF01557	39.8	78	197
HRADE27	867195	444	HMMER 2.1.1 blastx.2	PFAM: Asparagine synthase	pir G83604 G83604	55% 40%	197 12	346 188
HTXQR10	869137	445	HMMER 2.1.1 blastx.2	asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4) - Escherichia coli	pir A36616 AJECN	72% 98% 87%	270 31 589	656 267 636
HTXQR10	869137	445	HMMER 2.1.1 blastx.2	PFAM: Glycosyl transferases group 1 L165.1 (Fragment).	PF00534	25	125	403
HTXQR10	869137	445	HMMER 2.1.1 blastx.2	PFAM: Kelch motif	sp AAAF77213 AAAF77 213	40% 44%	50 385	409 531
HTXQR10	869137	445	HMMER 2.1.1 blastx.2	PFAM: Kelch motif	PF01344	94.1	283	423
HTXQR10	869137	445	HMMER 2.1.1 blastx.2	KELCH MOTIF CONTAINING PROTEIN.	sp Q9Y2M5 Q9Y2M 5	44% 32% 43% 34% 36%	166 166 181 166 181	381 531 366 381 363

[illegible]

HELBA42	878549	451	HMMER 2.1.1 blastx.2	PFAM: Acetyltransferase (GNAT) family hypothetical protein DKFZp564C103.1 - human	PF00583 pir T08699 T08699	37.5	384	560
HSPBB15	878791	452	HMMER 2.1.1 blastx.2	PFAM: GMC oxidoreductases Choline dehydrogenase (Fragment).	PF00732 sp CAB75961 CAB7 5961	100 99% 88% 55% 61%	196 482 145 3 101	480 955 480 176 205
HTAFF91	879399	453	HMMER 2.1.1 blastx.2	PFAM: RNB-like proteins	PF00773	88	9	404
HETHB58	879640	454	HMMER 2.1.1 blastx.2	EXORIBONUCLEASE, VACB/RNB FAMILY. PFAM: alpha/beta hydrolase fold CGI-58 PROTEIN.	sp Q9PK00 Q9PK00 PF00561 sp Q9Y369 Q9Y369	38% 35.4 52% 56%	9 49 49 3	416 657 669 50
HGBCU40	880328	455	HMMER 2.1.1 blastx.2	PFAM: Glycosyl transferases Brain cDNA, clone MNCb-1820.	PF00535 sp BAA97985 BAA9 7985	27.2 64%	354 180	479 527
HE9PR39	882939	456	HMMER 2.1.1 blastx.2	PFAM: Sialyltransferase family ALPHA-N- ACETYL GALACTOSA MINIDE ALPHA-2,6- SIALYLTRANSFERASE 1	PF00777 sp Q64686 CAG7_R AT	37.8 56%	330 93	452 614

HTEAF36	883195	872	HMMER 2.1.1	PFAM: DNA/RNA non-specific endonuclease	PF01223	148.3	274	636
HTLGW66	883855	458	HMMER 2.1.1	PFAM: Histone deacetylase family	PF00850	48.1	264	458
			blastx.2	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHD1).	sp Q9Z2V6 HDA5_MOUSE	59% 58% 41% 54%	3 619 903 171	605 1074 1085 236
HPJDV95	888844	459	HMMER 2.1.1	PFAM: HECT-domain (ubiquitin-transferase).	PF00632	233.1	971	1906
			blastx.2	CG4238 PROTEIN.	sp Q9VQ67 Q9VQ67	62% 27%	518 9	1906 341
HCROF75	889436	460	HMMER 2.1.1	PFAM: Isochorismatase family	PF00857	46.2	252	341
			blastx.2	hypothetical protein F35G2.2 - Caenorhabditis elegans	pir T21813 T21813	57% 48%	219 135	467 245
HDPAP15	909703	461	HMMER 2.1.1	PFAM: Glycosyl transferases group 1	PF00534	138.4	503	1051
			blastx.2	BA13B9.1 (novel protein similar to a 1	sp CAC07999 CAC07999	100% 85%	221 2	1120 79
HTGDH34	913378	873	HMMER 2.1.1	PFAM: Acetyltransferase (GNAT) family	PF00583	61.6	376	708
			blastx.14	(AF085355) N-terminal acetyltransferase complex ard1 subunit [Homo sapiens]	gi 5114045 gb AAD40190.1	86%	376	765
HPDEH29	914591	463	HMMER 2.1.1	PFAM: Myosin tail	PF01576	43.8	239	454

HDPVG08	914973	464	blastx.2	smooth muscle myosin heavy chain isoform SMemb - human (fragment)	pir I65769 I65769	57%	61	165
			HMMER 2.1.1	PFAM: UBA domain	PF00627	43.4	342	461
HFXDW32	916095	465	blastx.2	CG13472 PROTEIN.	sp Q9VUH8 Q9VUH8	35%	1419	1712
			HMMER 2.1.1	PFAM: Domain of unknown function	PF00990	70.4	464	652
HSSCY03	916445	466	blastx.2	probable membrane protein yciR - Escherichia coli	pir H64876 H64876	76%	356	730
			HMMER 2.1.1	PFAM: HECT-domain (ubiquitin-transferase).	PF00632	64%	705	875
HFXFI49	916758	467	blastx.2	giant protein p619 - human	pir S71752 S71752	30%	582	719
			HMMER 2.1.1	PFAM: Isochorismatase family	PF00857	96.5	764	1297
HTLGH72	917526	468	blastx.2	probable membrane protein ycaC - Escherichia coli	pir S09671 S09671	37%	311	1327
			HMMER 2.1.1	PFAM: Isochorismatase family	PF00857	62%	153	200
HFXFI49	916758	467	blastx.2	probable membrane protein ycaC - Escherichia coli	pir S09671 S09671	80	343	588
			HMMER 2.1.1	PFAM: Isochorismatase family	PF00857	100%	304	588
HTLGH72	917526	468	blastx.2	PFAM: Peptide methionine sulfoxide reductase	PF01625	353	267	746
			HMMER 2.1.1	PEPTIDE METHIONINE SULFOXIDE REDUCTASE (EC	sp Q9UJ68 Q9UJ68	99%	72	776

HSUAE63	917758	469	HMMER 2.1.1 blastx.2	1.8.4.6). PFAM: tRNA synthetase class II (G, H, P, S and T) threonine--tRNA ligase (EC 6.1.1.3) - human	PF00587	340.1	926	2110
					pir A38867 YSHUT	61% 39% 64%	1232 118 935	2188 891 1171
HAPTQ56	918920	470	HMMER 2.1.1 blastx.2	PFAM: Phosphotriesterase family PHOSPHOTRIESTERAS E RELATED PROTEIN (PARATHION 1)	PF02126	433.7	1250	618
					sp Q60866 PTER_M OUSE	88%	1241	606
HAPTQ56	919863	874	HMMER 2.1.1 blastx.14	PFAM: Phosphotriesterase family parathion hydrolase (phosphotriesterase)- related protein [Mus musculus]	PF02126	433.7	82	714
					gi 881499 gb AAA68 951.1	88%	91	726
HNFIF54	919034	471	HMMER 2.1.1 blastx.2	PFAM: FAD binding domain succinate dehydrogenase (EC 1.3.99.1) flavoprotein - Escherichia coli	PF00890	210.3	242	577
					pir B64808 DEECSE	92%	2	577
HSDFF02	920435	472	HMMER 2.1.1 blastx.2	PFAM: Ribonuclease T2 family Enterobacter ribonuclease (EC 3.1.27.6) I precursor - Escherichia coli	PF00445	42.9	2	151
					pir JQ0777 JQ0777	90% 95%	2 349	382 414
HE8NS06	921076	473	HMMER 2.1.1 blastx.2	PFAM: Acetyltransferase (GNAT) family P300/CBP-	PF00583	42.6	555	776
					sp Q92831 Q92831	90%	48	1025

HASBA77	921365	474	blastx.2	ASSOCIATED FACTOR.		98%	1060	1248
				PEPTIDE CHAIN RELEASE FACTOR 2 (RF-2).	sp Q53915 RF2_STR CO	100%	1	48
						45%	129	185
HASBA77	921366	875	HMMER 2.1.1	PFAM: Peptidyl-tRNA hydrolase domain	PF00472	26.5	295	435
			blastx.14	PrfB [Streptomyces coelicolor]	gi 1402638 dbj BAA1 3170.1	45%	247	438
HSKDP26	921831	475	HMMER 2.1.1	PFAM: Site-specific recombinases	PF00239	138.8	395	81
			blastx.2	probable resolvase b1545 - Escherichia coli	pir D64909 D64909	100%	395	51
						71%	466	404
HMTAY52	921948	476	HMMER 2.1.1	PFAM: Flavin containing amine oxidase	PF01593	78.3	224	451
			blastx.2	CDNA FLJ20746 FIS, CLONE HEP06040.	sp BAA91360 BAA9 1360	94%	125	880
						87%	998	1093
						77%	883	963
						68%	975	1022
HSDJG01	922453	477	HMMER 2.1.1	PFAM: HECT-domain (ubiquitin-transferase).	PF00632	105.2	121	612
			blastx.2	CYCLIN-E BINDING PROTEIN 1.	sp Q9UII4 Q9UII4	90%	7	789
						96%	2	100
HHEPF30	928000	478	HMMER 2.1.1	PFAM: HECT-domain (ubiquitin-transferase).	PF00632	428	1	585
			blastx.2	ubiquitin ligase Nedd4 - rat (fragment)	pir S70642 S70642	95%	1	588
HTLAB16	929948	479	HMMER 2.1.1	PFAM: Flavin containing amine oxidase	PF01593	74.7	274	918

HOHCW42	930431	480	blastx.2	CDNA FLJ20746 FIS, CLONE HEP06040.	sp BAA91360 BAA9 1360	49%	217	945
			HMMER 2.1.1	PFAM: HECT-domain (ubiquitin-transferase).	PF00632	35%	1	186
HCHNX75	931615	481	blastx.2	HYPOTHETICAL 47.0 KDA PROTEIN (FRAGMENT).	sp Q9UDU3 Q9UDU 3	236.1	2527	1634
			HMMER 2.1.1	PFAM: Kelch motif	PF01344	96%	2719	1634
HBCBA92	933093	482	blastx.2	CDNA FLJ10748 FIS, CLONE NT2RP3001819, WEAKLY SIMILAR TO 1	sp BAA91787 BAA9 1787	102.5	184	324
			HMMER 2.1.1	PFAM: alpha/beta hydrolase fold	PF00561	49%	34	714
HHFJ131	933110	483	blastx.2	Hypothetical 22.5 kDa protein.	sp CAB97209 CAB9 7209	27%	37	678
			HMMER 2.1.1	PFAM: tRNA synthetases class I (W and Y)	PF00579	27%	121	666
HTXNN68	933670	484	blastx.2	MITOCHONDRIAL TRYPTOPHANYL- TRNA SYNTHETASE PRECURSOR (EC 1	sp Q9UGM6 Q9UG M6	29%	262	669
			HMMER 2.1.1	PFAM: Glycosyl hydrolase family 47	PF01532	100%	123	512
HWWFW06	933671	485	blastx.2	hypothetical protein C47E12.3 - Caenorhabditis elegans	pir T20009 T20009	100%	15	512
			HMMER 2.1.1	PFAM: Glycosyl hydrolase family 47	PF01532	75%	494	577
						63%	577	609
						540.8	1	906
						64%	1	909
						159.3	78	320

HE2SY77	934771	486	blastx.2	hypothetical protein C47E12.3 - Caenorhabditis elegans	pir T20009 T20009	46%	78	530
			HMMER 2.1.1	PFAM: Biotin protein ligase	PF01317	115.6	24	299
			blastx.2	birA bifunctional protein [validated] - Escherichia coli	pir B24029 BVECBF	100% 100%	3 301	299 330
HSHCO49	934819	487	HMMER 2.1.1	PFAM: Putative undecaprenyl diphosphate synthase	PF01255	235.8	227	766
			blastx.2	CG10778 PROTEIN.	sp Q9W3M6 Q9W3 M6	49%	134	766
HMUBI13	937820	488	HMMER 2.1.1	PFAM: Fumarylacetoacetate (FAA) hydrolase family	PF01557	288.8	327	830
			blastx.2	Brain cDNA, clone MNCb-4134.	sp BAA95083 BAA9 5083	87%	237	899
HBXGL55	938766	489	HMMER 2.1.1	PFAM: Kelch motif	PF01344	150.2	1248	1388
			blastx.2	CDNA FLJ11078 FIS, CLONE PLACE1005102, WEAKLY SIMILAR TO 1	sp BAA91990 BAA9 1990	34% 34%	849 127	1838 756
HAFAH26	940254	490	HMMER 2.1.1	PFAM: alpha/beta hydrolase fold	PF00561	25.5	469	774
			blastx.2	BEM46 PROTEIN.	sp O76462 O76462	43%	214	1050
HARMG23	942860	491	HMMER 2.1.1	PFAM: tRNA synthetase class II (G, H, P, S and T)	PF00587	57.9	43	507
			blastx.2	CDNA FLJ20450 FIS,	sp BAA91176 BAA9	86%	43	612

HOFMV44	943224	492	HMMER 2.1.1	CLONE KAT05607. PFAM: Kelch motif	1176	100%	3	38
			blastx.2	CG6224 PROTEIN.	PF01344	294.3	863	1003
HE9CJ28	949245	493	HMMER 2.1.1	PFAM: Thif family	sp Q9VUU5 Q9VUU5	43%	2	1129
			blastx.2	CG1749 PROTEIN.	sp Q9VUY3 Q9VUY3	34%	65	1138
HE8AZ89	950713	494	HMMER 2.1.1	PFAM: IPP transferase	PF01715	39%	275	1012
			blastx.2	ttna isopentenyltransferase - fission yeast (Schizosaccharomyces pombe)	pir T38664 T38664	142.6	1143	694
HFXXKW94	950717	495	HMMER 2.1.1	PFAM: N- acetylmuramoyl-L-alanine amidase	PF01510	59%	1356	145
			blastx.2	hypothetical protein b0868 - Escherichia coli	pir D64825 D64825	143.2	179	628
HISAF41	951370	496	HMMER 2.1.1	PFAM: Glucosamine-6- phosphate isomerase	PF01182	38%	80	628
			blastx.2	probable glucosamine-6- phosphate isomerase (EC 5.3.1.10) - golden hamster	pir S68445 S68445	188.7	289	774
HDPJH11	951371	497	HMMER	PFAM: Glucosamine-6- phosphate isomerase	PF01182	99%	1769	1050
			blastx.2	PFAM: Glucosamine-6- phosphate isomerase	PF01182	90%	2044	1718
HDPJH11	951371	497	HMMER	PFAM: Glucosamine-6- phosphate isomerase	PF01182	100%	2096	2049
			blastx.2	PFAM: Glucosamine-6- phosphate isomerase	PF01182	39%	77	9
HDPJH11	951371	497	HMMER	PFAM: Glucosamine-6- phosphate isomerase	PF01182	253.8	1669	1331
			blastx.2	PFAM: Glucosamine-6- phosphate isomerase	PF01182	91%	1675	1232
HDPJH11	951371	497	HMMER	PFAM: Glucosamine-6- phosphate isomerase	PF01182	209.4	199	504
			blastx.2	PFAM: Glucosamine-6- phosphate isomerase	PF01182	209.4	199	504

			2.1.1	phosphate isomerase					
			blastx.2	probable glucosamine-6-phosphate isomerase (EC 5.3.1.10) - golden hamster	pir S68445 S68445	84%	130	492	
HLHCP93	951372	876	HMMER 2.1.1	PFAM: Glucosamine-6-phosphate isomerase	PF01182	230.7	244	567	
			blastx.2	unnamed protein product [unidentified]	emb CAA03416.1	80%	244	699	
HAIBC14	951671	499	HMMER 2.1.1	PFAM: Acetyltransferase (GNAT) family	PF00583	75%	87	197	
			blastx.2	Separation anxiety protein.	sp AAF34715 AAF34715	42.4	311	679	
						71%	299	796	
HKAJZ24	951676	500	HMMER 2.1.1	PFAM: Glycosyl transferases	PF00535	74	228	779	
			blastx.2	GALNAC-T5 (FRAGMENT).	sp Q9UGK7 Q9UGK7	93%	27	827	
						62%	758	805	
						81%	751	783	
HWADY95	951731	501	HMMER 2.1.1	PFAM: GMC oxidoreductases	PF00732	190.1	29	433	
			blastx.2	Choline dehydrogenase (Fragment).	sp CAB75961 CAB75961	100%	2	514	
HCHAG27	952058	502	HMMER 2.1.1	PFAM: alpha/beta hydrolase fold	PF00561	50.8	315	521	
			blastx.2	hypothetical protein R05D7.4 - Caenorhabditis elegans	pir T23932 T23932	42%	785	1084	
						38%	237	662	
HPCRA07	952124	503	HMMER 2.1.1	PFAM: Elongation factor G C-terminus	PF00679	50.1	99	224	
			blastx.2	U5-116 KDA.	sp O08810 O08810	91%	3	407	
HDMAF23	952729	504	HMMER	PFAM: Transglutaminase-	PF01841	46.6	1271	1116	

				2.1.1	like superfamily PNGase (Fragment).					
				blastx.2						
HRGBU12	952730	505		HMMER 2.1.1 blastx.2	PFAM: Transglutaminase- like superfamily PNGase (Fragment).	PFO1841	sp AAF74720 AAAF74 720	99%	1283	219
HADFED82	953295	506		HMMER 2.1.1 blastx.2	PFAM: Histone deacetylase family HISTONE DEACETYLASE 6 (HD6).	PF00850	sp AAF74720 AAAF74 720	98% 53% 62%	6 454 522	455 531 593
								309.6	118	996
HCGAF54	954048	507		HMMER 2.1.1 blastx.2	PFAM: ubiE/CQO5 methyltransferase family CG2453 PROTEIN.	PF01209	sp Q9UBN7 HDA6_ HUMAN	52% 53%	118 118	996 984
								133.3	217	423
HSLGA19	610031	508		blastx.2	glucosyltransferase (EC 2.4.1.-) I - Escherichia coli	pilB42595 B42595	pir B42595 B42595	96% 100% 100% 90%	4 585 275 466	285 866 475 588
								177.9	1901	1392
HSLGA19	955327	877		HMMER 2.1.1 blastx.2	PFAM: Glycosyl transferases group 1 lipopolysaccharide core biosynthesis protein [Escherichia coli]	PF00534	gb AAA24082.1	98%	6	860
HWWCL36	955759	509		HMMER 2.1.1 blastx.2	PFAM: tRNA synthetase class II (G, H, P, S and T) threonine-tRNA ligase	PF00587	pir A38867 YSHUT	222.3	5	610
								76%	2	658

HD TEN41	955895	510	HMMER 2.1.1 blastx.2	(EC 6.1.1.3) - human PFAM: Kelch motif	PF01344	380.6	1144	1284
HSDDD20	956046	511	HMMER 2.1.1 blastx.2	KEAP1 PROTEIN.	sp Q9Z2X8 Q9Z2X8	94%	169	1464
			HMMER 2.1.1 blastx.2	PFAM: alpha/beta hydrolase fold	PF00561	53.2	55	648
HDPBL08	959377	512	HMMER 2.1.1 blastx.2	probable hydrolase b1009 - Escherichia coli	pir G64842 G64842	87% 57%	1 651	702 734
			HMMER 2.1.1 blastx.2	PFAM: Rhodanese-like domain	PF00581	36.7	581	823
HMEIJ75	960354	513	HMMER 2.1.1 blastx.2	hypothetical protein DKFZp762H1311.1 - human (fragment)	pir T50634 T50634	78%	521	970
			HMMER 2.1.1 blastx.2	PFAM: Poly A polymerase family	PF01743	162.7	393	893
HLTCU08	960951	514	HMMER 2.1.1 blastx.2	CGI-47 PROTEIN.	sp Q9Y362 Q9Y362	95% 100%	153 1187	1187 1249
			HMMER 2.1.1 blastx.2	PFAM: Kelch motif	PF01344	214	516	656
HTOHK41	960955	515	HMMER 2.1.1 blastx.2	KELCH MOTIF CONTAINING PROTEIN.	sp Q9Y2M5 Q9Y2M5	39% 37% 37% 59%	48 69 75 1	677 650 677 66
			HMMER 2.1.1 blastx.2	PFAM: Kelch motif	PF01344	96.6	762	634
HTKAA03	961002	516	HMMER 2.1.1 blastx.2	LYMPHOCYTE ACTIVATION- ASSOCIATED PROTEIN.	sp Q9Y2X2 Q9Y2X2	27% 29% 25%	981 1002 1002	310 484 361
			HMMER	PFAM:	PF01557	89.9	2	148

				Fumarylacetoacetate (FAA) hydrolase family					
				probable 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase b1180 - Escherichia coli	pir A64864 A64864	98%	2	202	
HMSGF27	962420	517		HMMER 2.1.1 PFAM: Glycosyl hydrolase family 47	PF01532	38.1	198	323	
				blastx.2 CDNA FLJ10783 FIS, CLONE NT2RP4000417, WEAKLY SIMILAR TO 1	sp BAA91806 BAA91806	90% 34%	204 76	332 204	
HHFLM17	963511	518		HMMER 2.1.1 PFAM: Kelch motif	PF01344	151.1	69	212	
				blastx.2 ACTIN-BINDING PROTEIN.	sp Q9Y573 Q9Y573	100% 32% 30% 30% 30% 100% 54%	3 6 3 84 228 446 452	443 440 401 377 440 490 484	
HLICL10	964035	519		HMMER 2.1.1 PFAM: AhpC/TSA family	PF00578	247.1	108	575	
				blastx.2 ANTIOXIDANT PROTEIN 2 (EC 1.11.1.7) (24 KDA PROTEIN) 1	sp P30041 AOP2_HUMAN	100%	93	761	
HCUAZ04	965585	520		HMMER 2.1.1 PFAM: Fumarylacetoacetate (FAA) hydrolase family	PF01557	100.2	495	292	
				blastx.2 CGI-105 PROTEIN.	sp Q9Y3B0 Q9Y3B0	91%	546	214	

HE2SB11	965611	521	HMMER 2.1.1 blastx.2	PFAM: Glycosyl transferases group 1 CG11306 PROTEIN.	PF00534	33.4	160	375
HCFLJ17	954723	522	HMMER 1.8 blastx.2	PFAM: Helix-loop-helix DNA-binding domain NY-REN-6 ANTIGEN (FRAGMENT).	sp Q9VP06 Q9VP06 PF00010	55% 61% 8.34	154 126 151	438 164 207
HCFLJ17	966294	878	HMMER 2.1.1 blastx.2	PFAM: FF domain (AF155096) NY-REN-6 antigen [Homo sapiens]	sp Q9Y5A8 Q9Y5A8 PF01846	60% 94% 63.4	199 1 174	411 105 341
HLICJ19	966969	523	HMMER 2.1.1 blastx.2	PFAM: Acetyltransferase (GNAT) family EMeg32 protein.	gb AAD42862.1 AF1 55096_1 PF00583	99% 69% 27.2	3 1178 52	1193 1216 282
HDPSM18	967483	524	HMMER 2.1.1 blastx.2	PFAM: ThiF family Ubiquitin-activating enzyme E1.	sp CAA04463 CAA0 4463 PF00899	71% 26.4	1 193	321 279
HMAKJ82	967593	525	HMMER 2.1.1	PFAM: Kelch motif	sp BAA94076 BAA9 4076 PF01344	38% 41% 57% 42.7	1 246 407 286	279 347 448 429
HFPIX37	971428	526	HMMER 2.1.1 blastx.2	PFAM: Histone deacetylase family hypothetical protein DKFZp566E044.1 - human	PF00850 pir T46284 T46284	30.2 49% 43%	4 4 1	138 258 255
HHEKP47	974402	527	HMMER 2.1.1	PFAM: Acetyltransferase (GNAT) family	PF00583	102.6	111	497

				blastx.2	phnO protein - Escherichia coli	pir G35719 G35719	100%	96	527
HTPDV62	418671	528		HMMER 2.1.1	PFAM: Guanylate kinase	PF00625	41.6	2	109
				blastx.2	guanylate kinase (EC 2.7.4.8) 1 - human	pir S68864 S68864	100% 95%	2 200	109 268
HUSAJ73	567234	529		HMMER 2.1.1	PFAM: POLO box duplicated region.	PF00659	26.4	31	126
				blastx.2	SERUM-INDUCIBLE KINASE.	sp O60679 O60679	97% 88% 57%	31 415 488	159 492 589
HSKCJ76	747380	530		HMMER 2.1.1	PFAM: POLO box duplicated region.	PF00659	98	115	306
				blastx.2	SERUM-INDUCIBLE KINASE.	sp O60679 O60679	95% 100%	115 104	321 18
HCEOX38	881200	531		HMMER 2.1.1	PFAM: CNH domain	PF00780	68.9	105	386
				blastx.2	Misshapen/NIK-related kinase MINK-1.	sp BAA90753 BAA9 0753	95% 100%	120 3	386 53
HFICR59	911317	532		HMMER 2.1.1	PFAM: Guanylate kinase	PF00625	141.3	221	493
				blastx.2	MAGUK protein VAM-1.	sp AAD45919 AAD4 5919	100%	2	721
HPDVO67	911405	533		HMMER 2.1.1	PFAM: Guanylate kinase	PF00625	46.4	211	396
				blastx.2	ZO-3.	sp O95049 O95049	88% 59% 68% 50%	1 629 690 387	726 784 755 446
H2LAD53	952181	534		HMMER	PFAM: Guanylate kinase	PF00625	69.8	1	177

HETLM90	954181	535	2.1.1	PALS1.	sp AAF63789 AAF63789	100%	1	360
			blastx.2					
			HMMER 2.1.1	PFAM: CNH domain	PF00780	183.7	16	711
HCE5E94	971074	882	blastx.2	GERMINAL CENTER KINASE RELATED PROTEIN KINASE.	sp Q9Y6R5 Q9Y6R5	94%	1	771
			HMMER 2.1.1	PFAM: Deoxynucleoside kinase	PF01712	62.3	423	761
			blastx.14	(AF087661) NADH-ubiquinone oxidoreductase 42 kDa subunit [Homo sapiens]	gi 4191348 gb AAD09755.1	94%	33	1097
HFXCU55	499457	537	HMMER 2.1.1	PFAM: Semialdehyde dehydrogenase	PF01118	54.3	147	1
			blastx.2	aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) - Escherichia coli	pir A00364 DEECDA	100%	177	1
			HMMER 2.1.1	PFAM: Semialdehyde dehydrogenase	PF01118	53.4	211	378
HEPBV24	513261	538	blastx.2	aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) - Escherichia coli	pir A00364 DEECDA	89%	208	378
			HMMER 2.1.1	PFAM: Hydratase/decarboxylase	PF01689	97.3	52	204
			blastx.2	probable hydratase (EC 4.2.1.-) mhpD -	pir F64762 F64762	100% 98%	207 52	416 204

HTLBD23	527944	540	HMMER 2.1.1 blastx.2	Escherichia coli PFAM: Domain of unknown function enterobactin synthetase component F - Escherichia coli	PF00668 pir H64791 YGECEF	56% 70% 49	418 2 78	549 52 377
HCEBM51	536558	541	HMMER 2.1.1 blastx.2	PFAM: Proline dehydrogenase PROLINE OXIDASE, MITOCHONDRIAL PRECURSOR (EC 1.5.3.-) 1	PF01619 sp O43272 PROD_H UMAN	218.9 79% 100%	36 33 1	416 464 33
HSLFF79	609838	542	HMMER 2.1.1 blastx.2	PFAM: Glycosyl transferase probable undecaprenyl- phosphate 1 K-12)	PF00953 pir C65182 C65182	24.5 85%	88 82	231 741
HSLFF79	961693	883	HMMER 2.1.1 blastx.2	PFAM: Glycosyl transferase (AE000454) UDP- GlcNAc:undecaprenylpho sphate GlcNAc-1- phosphate 1 [Escherichia coli]	PF00953 gb AAC76789.1	20.6 100%	857 152	684 838
HKTAB71	661483	543	HMMER 2.1.1 blastx.2	PFAM: Glycine cleavage T-protein (aminomethyl transferase) DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC	PF01571 sp Q9UI17 Q9UI17	186.1 100%	9 9	350 374

HSDIF25	678003	544	HMMER 2.1.1	1.5.99.2). PFAM: Tetrahydrofolate dehydrogenase/cyclohydr olase	PF00763	282.6	51	425
			blastx.2	methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5) 1 - Escherichia coli	pir H64784 JS0662	98% 82%	45 409	425 495
HNHWW82	684342	545	HMMER 2.1.1	PFAM: Dehydratase family	PF00920	34.2	183	266
			blastx.2	probable dihydroxy-acid dehydratase yagF - Escherichia coli	pir E64752 E64752	90% 100% 70%	1 183 93	195 284 122
HFATN41	712097	546	HMMER 2.1.1	PFAM: Dihydroorotate dehydrogenase	PF01180	203.7	304	690
			blastx.2	dihydroorotate oxidase (EC 1.3.3.1) - Escherichia coli	pir A23109 DEECDO	87% 95%	298 18	729 296
HFFFG80	733387	547	HMMER 2.1.1	PFAM: Galactosyltransferase	PF01762	28.3	179	427
			blastx.2	T7N9.18.	sp AAF79857 AAF79 857	30%	8	478
HSDFF73	761657	548	HMMER 2.1.1	PFAM: Prephenate dehydratase	PF00800	75.3	3	200
			blastx.2	chorismate mutase (EC 5.4.99.5) / prephenate dehydratase (EC 4.2.1.51) pheA [validated] - Escherichia coli	pir A30261 KMECP W	82%	3	488
HTLBH79	774422	549	HMMER	PFAM:	PF01762	115.2	252	545

[illegible]

HMJAS41	827510	554	blastx.2 HMMER 2.1.1	KIDNEY AND LIVER PROLINE OXIDASE 1. PFAM: NAD-dependent glycerol-3-phosphate dehydrogenase	sp Q9UF12 Q9UF12 PF01210	91%	1	453
			blastx.2	GLYCEROL-3- PHOSPHATE DEHYDROGENASE [NAD+], CYTOPLASMIC 1	sp O57656 GPDA_F UGRU	66%	44	382
HTXOH20	837509	555	HMMER 2.1.1	PFAM: Glycosyl hydrolases family 35	PF01301	27.7	199	294
			blastx.2	CG3132 PROTEIN.	sp Q9VGE7 Q9VGE7 PF00549	37%	22	405
HSLFG13	847314	556	HMMER 2.1.1	PFAM: CoA-ligases		200.1	274	681
			blastx.2	succinate--CoA ligase (ADP-forming) (EC 6.2.1.5) alpha chain - Escherichia coli	pir A90499 SYECSA	79% 100%	187 3	681 185
HDAAS21	850577	557	HMMER 2.1.1	PFAM: PQQ enzyme repeat	PF01011	29.2	155	268
			blastx.2	serine/threonine protein kinase related protein - 1	pir H69064 H69064	31% 28% 25%	98 77 98	703 724 724
HARMH10	852701	558	HMMER 2.1.1	PFAM: Pyridoxamine 5'- phosphate oxidase	PF01243	119.7	362	685
			blastx.2	CDNA FLJ10535 FIS, CLONE NT2RP2001070, WEAKLY SIMILAR TO 1	sp BAA91668 BAA9 1668	97% 52%	269 685	700 810

HSDAI07	859237	559	HMMER 2.1.1 blastx.2	PFAM: Orn/Lys/Arg decarboxylase	PF01276	377.1	123	623
				ornithine decarboxylase (EC 4.1.1.17), inducible - Escherichia coli	pir A40839 A40839	85% 93%	3 35	623 121
HLDQU41	864996	560	HMMER 2.1.1 blastx.2	PFAM: Carbon-nitrogen hydrolase	PF00795	94.1	208	486
				BETA- UREIDOPROPIONASE.	sp Q9UIR3 Q9UIR3	99%	1	501
HAIJU06	864997	561	HMMER 2.1.1 blastx.2	PFAM: Carbon-nitrogen hydrolase	PF00795	290.1	164	880
				BETA- UREIDOPROPIONASE.	sp Q9UBR1 Q9UBR1	98%	137	937
HSLDO63	866332	562	HMMER 2.1.1 blastx.2	PFAM: Glycosyl hydrolases family 31	PF01055	149.9	21	512
				hypothetical 77.2 kD protein in glnA-fdhE intergenic region - Escherichia coli (strain K- 12)	pir A65193 A65193	100%	3	521
HNHAG26	866694	563	HMMER 2.1.1 blastx.2	PFAM: Biotin synthase	PF01792	424.2	266	775
				biotin synthetase (EC 2.8.1.-) - Escherichia coli	pir JC2517 SYECBB	82% 87% 86%	2 90 2	880 260 112
HGBGC61	867065	564	HMMER 2.1.1 blastx.2	PFAM: Bacterial Cytochrome Ubiquinol Oxidase	PF01654	39.3	339	419
				cytochrome d ubiquinol oxidase (EC 1.10.3.-)	pir D64809 D64809	91% 100%	196 3	336 113

HMAEM27	870252	565	chain I - Escherichia coli	PFAM: tRNA synthetases class I (R)	PF00750	100%	339	419
HEBCK42	875541	566	HMMER 2.1.1	blastx.2	sp Q9VXT0 Q9VXT0	100%	116	208
			HMMER 2.1.1	blastx.2	PF00719	81%	419	451
			HMMER 2.1.1	blastx.2	pir A45153 A45153	24.6	531	716
HELFN03	881180	567	HMMER 2.1.1	blastx.2	PF00795	31%	291	716
			HMMER 2.1.1	blastx.2	PF00795	69.7	317	445
			HMMER 2.1.1	blastx.2	PF00795	100%	317	445
HKIMF95	882308	568	HMMER 2.1.1	blastx.2	pir H64796 H64796	64.3	461	733
			HMMER 2.1.1	blastx.2	PF01089	93%	383	733
			HMMER 2.1.1	blastx.2	pir T23765 T23765	41.1	46	222
HTLHE85	883263	569	HMMER 2.1.1	blastx.2	PF00744	46%	49	222
			HMMER 2.1.1	blastx.2	sp CAB95124 CAB95124	132.7	1	549
			HMMER 2.1.1	blastx.2	PF00852	91%	1	582
HTEOE72	886412	570	HMMER 2.1.1	blastx.2	PF00852	72%	515	721
			HMMER 2.1.1	blastx.2	sp Q9VLC1 Q9VLC1	83.4	115	498
			HMMER 2.1.1	blastx.2	PF00694	47%	100	600
HELBN13	907599	571	HMMER 2.1.1	blastx.2	PF00694	178.3	330	626
			HMMER 2.1.1	blastx.2	sp P25516 ACO1_EC	100%	330	644
			HMMER 2.1.1	blastx.2	PF00694	100%	330	644

HFUE03	914882	572		HYDRATASE 1 (EC 4.2.1.3) (CITRATE HYDRO-LYASE 1)	OLI	89%	106	354
			HMMER 2.1.1	PFAM: RNA pseudouridylate synthase	PF00849	94%	2	112
			blastx.2	HYPOTHETICAL 24.4 KDA PROTEIN IN LPD 3'REGION (ORF4).	sp O66114 YLP4_ZY MMO	100%	659	715
HABGE01	915743	573	HMMER 2.1.1	PFAM: tRNA synthetases class II (A)	PF01411	46.4	1708	1352
			blastx.2	CG10802 PROTEIN.	sp Q9W4R9 Q9W4R9	47%	1456	1313
HWLKM02	917409	574	HMMER 2.1.1	PFAM: Metallo-beta-lactamase superfamily	PF00753	36%	1705	1565
			blastx.2	hydroxyacylglutathione hydrolase (EC 3.1.2.6) - rat	pir JC5826 JC5826	48	362	739
HOVEB13	917564	575	HMMER 2.1.1	PFAM: Formate--tetrahydrofolate ligase	PF01268	53%	224	901
			blastx.2	hypothetical protein DKFZp586G1517.1 - human (fragment)	pir T17244 T17244	397.5	230	904
HE8UB94	920288	576	HMMER 2.1.1	PFAM: Protein-L-isoaspartate(D-aspartate) O-methyltransferase (PCMT)	PF01135	100%	242	904
			blastx.2	CDNA FLJ10883 FIS, CLONE NT2RP4001946, WEAKLY SIMILAR TO 1	sp BAA91877 BAA91877	55%	96	263
						25.3	235	369
						86%	211	516

HTHDJ23	921274	577	HMMER 2.1.1 blastx.2	PFAM: PQQ enzyme repeat Genomic DNA, chromosome 5, BAC clone:F14A1.	PF01011 sp BAA97455 BAA9 7455	32.4	1404	1505
HWHPB72	922580	578	HMMER 2.1.1 blastx.2	PFAM: tRNA synthetases class I (R) probable arginyl-trna synthetase, cytoplasmic - fission yeast (Schizosaccharomyces pombe)	PF00750 pir T39985 T39985	55.6 45%	499 472	687 702
HSQFX64	922581	579	HMMER 2.1.1 blastx.2	PFAM: tRNA synthetases class I (R) DJ382I10.5.1 (novel protein similar to arginyl- tRNA 1 1	PF00750 sp CAB76858 CAB7 6858	30.8 93% 60%	40 19 329	288 264 412
HDABB84	922582	580	HMMER 2.1.1 blastx.2	PFAM: tRNA synthetases class I (R) DJ382I10.5.1 (novel protein similar to arginyl- tRNA 1 1	PF00750 sp CAB76858 CAB7 6858	374.8 96%	291 594	1760 1760
HLHFN83	924110	581	HMMER 2.1.1 blastx.2	PFAM: Short chain dehydrogenase/reductase C-terminus Alcohol dehydrogenase, short chain.	PF00678 sp CAB89810 CAB8 9810	45.2 98%	45 3	137 224
HPCRR26	926401	582	HMMER 2.1.1 blastx.2	PFAM: CoA-ligases SUCCINYL-COA	PF00549 sp Q9UNP6 Q9UNP6	242.6 78%	750 819	295 280

HCMSD61	927475	583	HMMER 2.1.1 blastx.2	SYNTHETASE ALPHA SUBUNIT (EC 6.2.1.5). PFAM: Metallo-beta- lactamase superfamily	PF00753	44.4	153	692
HCEEC58	933866	584	HMMER 2.1.1 blastx.2	hypothetical protein CGI- 83 [imported] - human PFAM: NAD-dependent glycerol-3-phosphate dehydrogenase	pir T44603 T44603 PF01210	94% 183.1	105 1	959 324
HSYAD06	935334	585	HMMER 2.1.1 blastx.2	GLYCEROL-3- PHOSPHATE DEHYDROGENASE (NAD(P)+) (FRAGMENT). PFAM: Tetrahydrofolate dehydrogenase/cyclohydr olase	sp O02855 O02855 PF00763	78% 79.1	4 253	324 585
HUSID53	943374	586	HMMER 2.1.1 blastx.2	hypothetical protein DKFZp586G1517.1 - human (fragment) PFAM: Glycosyl hydrolases family 31	pir T17244 T17244 PF01055	97% 501.7	124 17	747 982
HRGDE77	948737	587	HMMER 2.1.1 blastx.2	GLUCOSIDASE II. PFAM: Metallo-beta- lactamase superfamily	sp P79403 P79403 PF00753	57% 44.3	17 530	958 769
HEGAU68	950009	588	HMMER 2.1.1	Brain cDNA, clone MNCb-5687, similar to Homo sapiens 1 PFAM: Glycosyl hydrolases family 35	sp BAA95092 BAA9 5092 PF01301	80% 132.8	8 17	1051 385

HNGKH38	951032	589	blastx.2	CG3132 PROTEIN.	sp Q9VGE7 Q9VGE7	59% 40%	2 311	196 496
HNHNN26	952398	590	HMMER 2.1.1	PFAM: Delta 1-pyrroline- 5-carboxylate reductase	PF01089	46.8	3	209
			blastx.2	CG5840 PROTEIN.	sp Q9VEJ3 Q9VEJ3	43%	12	212
			HMMER 2.1.1	PFAM: Magnesium chelate, subunit ChII	PF01078	91.1	161	406
HTEHP64	953791	591	blastx.2	hypothetical 56.2K protein (ilvG-rnC intergenic region) - Escherichia coli	pir JQ0872 JQ0872	85% 78% 72%	161 33 8	406 158 40
			HMMER 2.1.1	PFAM: Asparaginase	PF01112	32.1	198	404
			blastx.2	asparaginase (EC 3.5.1.1) [validated] - tree lupine (fragment)	pir S22523 S22523	40% 48% 58% 36%	3 294 101 333	281 497 202 407
HMIAO78	953793	592	HMMER 2.1.1	PFAM: Asparaginase	PF01112	71.3	316	486
			blastx.2	Putative l-asparaginase.	sp CAC09349 CAC0 9349	56% 40% 32%	316 162 482	486 326 577
			HMMER 2.1.1	PFAM: CDP-alcohol phosphatidyltransferase	PF01066	94.1	366	830
HFPCN94	955009	593	blastx.2	DJ967N21.6 (NOVEL CDP-ALCOHOL PHOSPHATIDYLTRAN SPERASE FAMILY 1	sp Q9UJA2 Q9UJA2	77%	84	860
			HMMER 2.1.1	PFAM: Gamma- glutamyltranspeptidase	PF01019	30.8	77	166
			HMMER 2.1.1					

			blastx.2	gamma-glutamyltransferase (EC 2.3.2.2) precursor - <i>Escherichia coli</i>	pir JV0028 EKECEX	66%	17	166
HPD VW40	961039	595	HMMER 2.1.1	PFAM: Adenylosuccinate synthetase	PF00709	458.6	6	533
			blastx.2	ADENYLOSUCCINATE SYNTHETASE, MUSCLE ISOZYME (EC 6.3.4.4) 1	sp P28650 PUA1_MOUSE	88%	3	629
HEMFC70	961963	596	HMMER 2.1.1	PFAM: Ubiquitin carboxyl-terminal hydrolase, family 1	PF01088	32.5	664	798
			blastx.2	AD-019 protein.	sp AAF67486 AAF67486	99%	217	1164
HLDOO20	910371	597	HMMER 1.8	PFAM: Core histones H2A, H2B, H3 and H4	PF00125	9.29	132	52
HLDOO20	963284	886	HMMER 2.1.1	PFAM: Urocanase	PF01175	175.9	12	1205
			blastx.14	urocanate hydratase [Trifolium repens]	gi 21965 emb CAA48765.1	32%	747	1196
						31%	12	269
						38%	543	692
						60%	282	326
						24%	327	485
HLDOO20	963655	887	HMMER 2.1.1	PFAM: Urocanase	PF01175	165	1	1188
			blastx.14	urocanate hydratase [Trifolium repens]	gi 21965 emb CAA48765.1	32%	730	1179
						38%	526	675
						29%	1	252
						60%	265	309

HSLEP67	963505	598	HMMER 2.1.1 blastx.2	PFAM: ThiJ/PfpI family	PF01965	52.9	107	238
				hydroxymethylpyrimidine kinase (EC 2.7.1.49) - Escherichia coli	pir H64771 H64771	98% 75%	113 76	352 123
HSLEP94	964463	599	HMMER 2.1.1 blastx.2	PFAM: Asparaginase	PF01112	543.1	444	1292
				probable asparaginase (EC 3.5.1.1) ybik - Escherichia coli	pir D64820 D64820	94% 93%	441 1292	1292 1336
HSENS89	964527	600	HMMER 2.1.1 blastx.2	PFAM: Formate-- tetrahydrofolate ligase	PF01268	637.3	43	876
				hypothetical protein DKFZp586G1517.1 - human (fragment)	pir T17244 T17244	75%	37	1050
HNTAF77	966190	601	HMMER 2.1.1 blastx.2	PFAM: Peptidyl-tRNA hydrolase	PF01195	100.1	3	275
				aminoacyl-tRNA hydrolase (EC 3.1.1.29) - Synechocystis sp. (strain PCC 6803)	pir S75738 S75738	52%	3	215
HBIOV48	967566	602	HMMER 2.1.1 blastx.2	PFAM: Gamma- glutamyltranspeptidase	PF01019	55.3	295	450
				DJ18C9.2 (NOVEL GENE (LOCUS D20S101) SIMILAR TO 1 1	sp Q9UJ14 Q9UJ14	84% 76% 55% 73%	148 65 6 468	450 154 107 530
HBMN45	967744	603	HMMER 2.1.1 blastx.2	PFAM: Oxidoreductase family	PF01408	129.4	2	454
				ycjS protein - Escherichia	pir F64880 F64880	84%	2	688

HBXCE20	970889	604	HMMER 2.1.1 blastx.2	coli PFAM: MoaC family	PF01967	178.9	116	370
				molybdenum cofactor biosynthesis protein C [validated] - Escherichia coli	pir G64814 G64814	80%	44	403
HSLJU88	780811	605	HMMER 2.1.1 blastx.2	PFAM: tRNA synthetases class I (E and Q)	PF00749	26.3	448	537
				dihydroorotate oxidase (EC 1.3.3.1) - Escherichia coli	pir A23109 DEECDO	100%	449	3
HKGDQ60	863330	606	HMMER 2.1.1 blastx.2	PFAM: tRNA synthetases class I (E and Q)	PF00749	193.4	114	458
				CG4573 PROTEIN.	sp Q9VV59 Q9VV59	63% 47%	117 460	446 750
HSDKF67	933059	607	HMMER 2.1.1 blastx.2	PFAM: tRNA synthetases class I (E and Q)	PF00749	274.1	2	451
				glutamine-tRNA ligase (EC 6.1.1.18) [validated] - Escherichia coli	pir G64802 SYECQT	98%	2	451
HSLFT94	603023	608	HMMER 2.1.1 blastx.2	PFAM: PAP2 superfamily	PF01569	72.8	15	302
				phosphatidylglycerophosph atase (EC 3.1.3.27) B - Escherichia coli	pir A30193 PAECGB	100%	3	314
HTJMD06	837603	609	HMMER 2.1.1	PFAM: Inositol polyphosphate phosphatase family, catalytic domain	PF00783	246.8	20	424

HNTBH68	851274	610	blastx.2	SYNAPTOJANIN 2 (EC 3.1.3.56) (SYNAPTIC 11	sp O15056 SYJ2_HU MAN	97%	14	433
			HMMER 2.1.1	PFAM: PAP2 superfamily	PF01569	100%	435	455
HMEKO39	863507	611	blastx.2	CDNA FLJ20300 FIS, CLONE HEP06465.	sp BAA91072 BAA9 1072	50.6	16	420
			HMMER 2.1.1	PFAM: PAP2 superfamily	PF01569	57%	1	540
HAABH11	965473	612	blastx.2	CDNA FLJ20300 FIS, CLONE HEP06465.	sp BAA91072 BAA9 1072	26.2	269	550
			HMMER 2.1.1	PFAM: PAP2 superfamily	PF01569	49%	2	619
HUVFZ43	910860	613	blastx.2	CG12746 PROTEIN.	sp Q9VND5 Q9VND 5	38.2	298	663
			HMMER 2.1.1	PFAM: Dual specificity phosphatase, catalytic domain	PF00782	46%	46	666
HCEPH84	910864	614	blastx.2	MAP kinase phosphatase.	sp BAA89534 BAA8 9534	164.4	6	401
			HMMER 2.1.1	PFAM: Dual specificity phosphatase, catalytic domain	PF00782	56%	3	494
HNFDO52	916260	615	blastx.2	PROTEIN PHOSPHATASE.	sp Q9UII6 Q9UII6	136.4	1158	727
			HMMER 2.1.1	PFAM: Dual specificity phosphatase, catalytic domain	PF00782	50%	1251	757
			blastx.2	dual specificity phosphoprotein phosphatase (EC 3.1.3.-) 2	pir A57126 A57126	92.1	2	358
			HMMER 2.1.1			95%	257	130
						100%		358

HHEJR23	919082	616	HMMER 2.1.1	- human PFAM: Dual specificity phosphatase, catalytic domain	PF00782	52.2	426	253
HMTAX31	971343	617	blastx.2	CG10371 PROTEIN.	sp Q9VCI6 Q9VCI6	42%	774	259
			HMMER 2.1.1	PFAM: Dual specificity phosphatase, catalytic domain	PF00782	176.8	1064	651
HKIYI74	729217	618	blastx.2	Mitogen-activated protein kinase phosphatase x.	sp AAF86649 AAF86 649	100%	1073	522
			HMMER 2.1.1	PFAM: metalloproteinase family M24	PF00557	67.5	6	251
			blastx.2	CG5188 PROTEIN.	sp Q9VKV9 Q9VKV 9	51% 61%	9 253	251 291
HSKEI21	760792	619	HMMER 2.1.1	PFAM: Aminopeptidase I zinc metalloprotease (M18)	PF02127	118.8	201	398
			blastx.2	ASPARTYL AMINOPEPTIDASE.	sp Q9ULA0 Q9ULA0	90%	138	473
HKAFK68	869127	620	HMMER 2.1.1	PFAM: Aminopeptidase I zinc metalloprotease (M18)	PF02127	190.4	216	506
			blastx.2	CDNA FLJ10915 FIS, CLONE OVARC1000288, WEAKLY SIMILAR TO 1	sp BAA91903 BAA9 1903	98% 92% 46%	117 529 506	506 570 589
HSRBB92	905110	621	HMMER 2.1.1	PFAM: UBX domain	PF00789	119.9	1757	2005
			blastx.2	CGI-03 PROTEIN (FAS-	sp Q9Y2Z3 Q9Y2Z3	93%	62	2011

HWLLR80	931564	622	HMMER 2.1.1 blastx.2	ASSOCIATED FACTOR, FAF1). PFAM: Cytosol aminopeptidase family CG7340 PROTEIN.	PF00883	245.2	1	522
HWLWQ87	932577	623	HMMER 2.1.1 blastx.2	PFAM: metalloproteinase family M24 PUTATIVE METHIONINE AMINOPEPTIDASE 1 (EC 3.4.11.18) 1	sp Q9V3D8 Q9V3D8 PF00557	69% 150	10 154	543 468
H6EEP53	942872	624	HMMER 2.1.1 blastx.2	PFAM: Insulinase (Peptidase family M16) MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT 1	sp P53582 AMP1_H UMAN	96% 66%	148 1	519 150
HE2KZ56	968439	625	HMMER 2.1.1 blastx.2	PFAM: metalloproteinase family M24 X-Pro dipeptidase (EC 3.4.13.9) - Escherichia coli (strain K-12) PFAM: RNase3 domain.	PF00557	88.8	100	315
HFXHD52	883683	888	HMMER 2.1.1	PFAM: HECT-domain (ubiquitin-transferase).	pir H65189 H65189	84%	1	342
HPMAM67	959570	889	HMMER 2.1.1 blastx.2	transcription/repair- coupling protein - Escherichia coli	PF00636	33.6	13	207
HBXFI75	566766	628	HMMER	PFAM: DEAD/DEAH	PF00632	65.3	246	440
HBXFI75	847655	892	HMMER		pir G64855 G64855	100% 91%	609 41	1295 601
					PF00270	68.3	1624	1869

HEJGM94	913938	629	2.1.1 HMMER 1.8	box helicase. PFAM: Elongation factor Tu family (contains ATP/GTP binding P-loop)	PF00009	442.48	244	1344
			blastx.2	ELONGATION FACTOR TU, MITOCHONDRIAL PRECURSOR (P43).	sp P49411 EFTU_HU MAN	89%	112	1437
HLJDQ52	923110	630	HMMER 2.1.1 blastx.2	PFAM: DEAD/DEAH box helicase CG4152 PROTEIN.	PF00270	77	405	785
					sp Q9Y134 Q9Y134	63% 61%	207 790	788 930
HAJAW40	1219455	631	blastx.2	RNA helicase Gu - human (fragment)	pir PC6010 PC6010	66% 22%	470 233	2122 556
HAJAW40	825697	893	HMMER 1.8	PFAM: DEAD and DEAH box helicases	PF00270	57.85	490	702
HATAZ67	1106635	632	blastx.2	RNA helicase - mouse	pir 49731 49731	59%	182	688
HATAZ67	908326	894	HMMER 1.8 blastx.14	PFAM: DEAD and DEAH box helicases RNA helicase [Mus musculus]	PF00270 gi 407992 gb AAA53 629.1	159.42 69% 50%	309 177 799	803 788 852
HBUAC02	1220017	633	blastx.2	Phorbol I protein.	sp AAF86650 AAF86 650	94% 100%	99 611	650 976
HBUAC02	933546	895	HMMER 1.8	PFAM: Cytidine and deoxycytidylate deaminases zinc-binding region (AL022318) bK150C2.3 (PUTATIVE novel protein 1 Phorbol) [Homo sapiens]	PF00383	24.31	294	416
			blastx.14		gi 5102832 emb CAB 45271.1	100%	57	599

HCWEQ14	.1117318	634	blastx.2	CDNA FLJ10432 FIS, CLONE NT2RP1000470, WEAKLY SIMILAR TO 1	sp BAA91606 BAA9 1606	100% 66%	43 5	177 40
HCWEQ14	908245	896	HMMER 1.8	PFAM: DEAD and DEAH box helicases	PF00270	72.08	37	177
HDPWH41	1228148	635	blastx.14	(AC002985) R27090_2 [Homo sapiens]	gi 2443870 gb AAB8 1544.1	100% 66%	37 5	177 40
HDPWH41	772569	897	blastx.2	CG9630 PROTEIN.	sp Q9VHU1 Q9VHU 1	49% 51%	94 618	615 1079
HDQEH61	1213567	636	HMMER 1.8	PFAM: DEAD and DEAH box helicases	PF00270	129.65	28	333
HDQEH61	908303	898	blastx.2	DEAD-BOX PROTEIN.	sp Q9Y659 Q9Y659	92% 71%	163 863	915 904
HDTDD72	587710	637	HMMER 1.8	PFAM: DEAD and DEAH box helicases	PF00270	181.89	221	760
HFRBN02	1152485	638	blastx.14	(AF106019) DEAD-box protein [Homo sapiens]	gi 5359631 gb AAD4 2744.1 AF106019_1	97% 71%	62 762	763 803
HFRBN02	973667	899	HMMER 1.8	PFAM: ATP synthase A chain	PF00119	85.33	165	350
HFRBN02	973667	899	blastx.2	H+-transporting ATP synthase (EC 3.6.1.34) protein 6 - 1	pir F59153 F59153	66% 86%	3 356	347 400
HFRBN02	973667	899	blastx.2	H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - Escherichia coli	pir G65176 PWECA	93%	2	967
HFRBN02	973667	899	HMMER 1.8	PFAM: ATP synthase alpha and beta subunits	PF00006	159.91	65	403
HFRBN02	973667	899	blastx.14	papA [Escherichia coli]	gi 42283 emb CAA23	86%	2	403

HKAIH72	1107045	639	blastx.2	DNA POLYMERASE THETA (EC 2.7.7.7) (DNA POLYMERASE ETA).	596.1	100% 40%	406 574	651 633
HKAIH72	761293	900	HMMER 1.8	PFAM: DNA polymerase family A	PF00476	90.98	55	522
HMAAD90	1152487	640	blastx.2	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain NDUFA3 - human	pir JE0379 JE0379	100%	8	250
HMAAD90	963983	901	HMMER 2.1.1	PFAM: ATP:guanine phosphotransferase	PF00217	932.7	1352	180
			blastx.14	sarcomeric mitochondrial creatine kinase precursor (EC 2.7.3.2) [Homo sapiens]	gi 338237 gb AAA60 561.1	100% 100%	1199 1427	171 1392
HMABQ71	1105540	641	blastx.2	DNA GYRASE SUBUNIT B (EC 5.99.1.3).	sp P06982 GYRB_E COLI	95% 96% 52%	317 562 70	60 308 2
HMABQ71	729831	902	HMMER 2.1.1	PFAM: DNA topoisomerase II (N- terminal region)	PF00204	128.8	210	407
HPJEV95	929723	903	HMMER 1.8	PFAM: ATP synthase A chain	PF00119	20.61	169	393
HSKYR59	1219545	643	blastx.2	H+-transporting ATP synthase (EC 3.6.1.34) delta chain precursor - human	pir S22348 S22348	90%	639	181
HSKYR59	933750	904	HMMER	PFAM: ATP synthase,	PF00401	116.4	13	342

HSWAM16	1151512	644	2.1.1 blastx.2	Delta/Epsilon chain H ⁺ -transporting ATP synthase (EC 3.6.1.34) delta chain precursor - human	pir S22348 S22348	90%	146	604
HSWAM16	933749	905	HMMER 2.1.1 blastx.14	PFAM: ATP synthase, Delta/Epsilon chain H(+)-transporting ATP synthase [Homo sapiens]	PF00401 gi 12586 emb CAA45 016.1	148.1 90%	206 146	586 604
HSXCW82	1164013	645	blastx.2	DEAD-BOX PROTEIN ABSTRAKT HOMOLOG.	sp Q9UTV9 ABS_HU MAN	96% 85%	147 7	1442 48
HSXCW82	739372	906	HMMER 1.8	PFAM: DEAD and DEAH box helicases	PF00270	92.34	142	387
HSYDB42	933545	646	HMMER 1.8	PFAM: Cytidine and deoxycytidylate deaminases zinc-binding region	PF00383	24.68	257	379
HTXKJ79	1193059	647	blastx.2	Phorbolin I protein.	sp AAF86650 AAF86 650	94% 100%	62 574	613 939
HTXKJ79	938963	907	blastx.2	H ⁺ -transporting ATP synthase (EC 3.6.1.34) lipid-binding protein P3 precursor, mitochondrial - human	pir J38612 J38612	80% 84%	107 1055	421 1186
HTXKJ79	938963	907	HMMER 1.8 blastx.14	PFAM: ATP synthase subunit C mitochondrial ATP synthase subunit 9 precursor [Homo sapiens]	PF00137 gi 511450 gb AAA78 807.1	38.73 80%	312 108	422 422

HUSGQ19	1165320	648	blastx.2	CG9630 PROTEIN.	sp Q9VHU1 Q9VHU1	48% 49% 46% 25%	559 35 1205 1413	1221 556 1411 1508
HUSGQ19	772568	908	HMMER 1.8	PFAM: DEAD and DEAH box helicases	PF00270	151.79	77	484
HUSZS75	1193982	649	blastx.2	CDNA FLJ11282 FIS, CLONE PLACE1009476, WEAKLY SIMILAR TO 1	sp BAA92106 BAA92106	100% 100% 100%	238 31 459	459 153 518
HUSZS75	908443	909	HMMER 1.8 blastx.14	PFAM: DEAD and DEAH box helicases (AC004531) Gene with similarity to DEAD box helicases [Homo sapiens]	PF00270	93.7	505	792
HWBDR25	1174365	650	blastx.2	probable RNA helicase - human	pir T08745 T08745	97%	12	1220
HWBDR25	659873	910	HMMER 1.8	PFAM: DEAD and DEAH box helicases	PF00270	170.59	24	416
HGSS51	954855	651	HMMER 2.1.1	PFAM: Cytidine and deoxycytidylate deaminase zinc-binding region	PF00383	34	66	173
			blastx.14	(AL117202) predicted using Genefinder; preliminary 1	gi 5832838 emb CAB55073.1	56% 41%	75 216	206 266

[51] Table 2 further characterizes certain encoded polypeptides of the invention, by providing the results of comparisons to protein and protein family databases. The first column provides a unique clone identifier, "Clone ID NO:", corresponding to a cDNA clone disclosed in Table 1A. The second column provides the unique contig identifier, "Contig ID:" which allows correlation with the information in Table 1A. The third column provides the sequence identifier, "SEQ ID NO:", for the contig polynucleotide sequences. The fourth column provides the analysis method by which the homology/identity disclosed in the Table was determined. The fifth column provides a description of the PFAM/NR hit identified by each analysis. Column six provides the accession number of the PFAM/NR hit disclosed in the fifth column. Column seven, score/percent identity, provides a quality score or the percent identity, of the hit disclosed in column five. Comparisons were made between polypeptides encoded by polynucleotides of the invention and a non-redundant protein database (herein referred to as "NR"), or a database of protein families (herein referred to as "PFAM"), as described below.

[52] The NR database, which comprises the NBRF PIR database, the NCBI GenPept database, and the SIB SwissProt and TrEMBL databases, was made non-redundant using the computer program nrdb2 (Warren Gish, Washington University in Saint Louis). Each of the polynucleotides shown in Table 1A, column 3 (e.g., SEQ ID NO:X or the 'Query' sequence) was used to search against the NR database. The computer program BLASTX was used to compare a 6-frame translation of the Query sequence to the NR database (for information about the BLASTX algorithm please see Altshul et al., J. Mol. Biol. 215:403-410 (1990); and Gish and States, Nat. Genet. 3:266-272 (1993). A description of the sequence that is most similar to the Query sequence (the highest scoring 'Subject') is shown in column five of Table 2 and the database accession number for that sequence is provided in column six. The highest scoring 'Subject' is reported in Table 2 if (a) the estimated probability that the match occurred by chance alone is less than $1.0\text{e-}07$, and (b) the match was not to a known repetitive element. BLASTX returns alignments of short polypeptide segments of the Query and Subject sequences which share a high degree of similarity; these segments are known as High-Scoring Segment Pairs or HSPs. Table 2 reports the degree of similarity between the Query and the Subject for each HSP as a percent identity in Column 7. The percent identity is determined by dividing the number of exact matches between the two aligned sequences in the HSP, dividing by the number of Query amino acids in the HSP

and multiplying by 100. The polynucleotides of SEQ ID NO:X which encode the polypeptide sequence that generates an HSP are delineated by columns 8 and 9 of Table 2.

[53] The PFAM database, PFAM version 2.1, (Sonnhammer et al., Nucl. Acids Res., 26:320-322, 1998)) consists of a series of multiple sequence alignments; one alignment for each protein family. Each multiple sequence alignment is converted into a probability model called a Hidden Markov Model, or HMM, that represents the position-specific variation among the sequences that make up the multiple sequence alignment (see, e.g., Durbin et al., *Biological sequence analysis: probabilistic models of proteins and nucleic acids*, Cambridge University Press, 1998 for the theory of HMMs). The program HMMER version 1.8 (Sean Eddy, Washington University in Saint Louis) was used to compare the predicted protein sequence for each Query sequence (SEQ ID NO:Y in Table 1A) to each of the HMMs derived from PFAM version 2.1. A HMM derived from PFAM version 2.1 was said to be a significant match to a polypeptide of the invention if the score returned by HMMER 1.8 was greater than 0.8 times the HMMER 1.8 score obtained with the most distantly related known member of that protein family. The description of the PFAM family which shares a significant match with a polypeptide of the invention is listed in column 5 of Table 2, and the database accession number of the PFAM hit is provided in column 6. Column 7 provides the score returned by HMMER version 1.8 for the alignment. Columns 8 and 9 delineate the polynucleotides of SEQ ID NO:X which encode the polypeptide sequence which show a significant match to a PFAM protein family.

[54] As mentioned, columns 8 and 9 in Table 2, "NT From" and "NT To", delineate the polynucleotides of "SEQ ID NO:X" that encode a polypeptide having a significant match to the PFAM/NR database as disclosed in the fifth column. In one embodiment, the invention provides a protein comprising, or alternatively consisting of, a polypeptide encoded by the polynucleotides of SEQ ID NO:X delineated in columns 8 and 9 of Table 2. Also provided are polynucleotides encoding such proteins, and the complementary strand thereto.

[55] The nucleotide sequence SEQ ID NO:X and the translated SEQ ID NO:Y are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and described further below. For instance, the nucleotide sequences of SEQ ID NO:X are useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in Clone ID NO:Z. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling

immediate applications in chromosome mapping, linkage analysis, tissue identification and/or typing, and a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y may be used to generate antibodies which bind specifically to these polypeptides, or fragments thereof, and/or to the polypeptides encoded by the cDNA clones identified in, for example, Table 1A.

[56] Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).

[57] Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X, and a predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing cDNA Clone ID NO:Z (deposited with the ATCC on October 5, 2000, and receiving ATCC designation numbers PTA 2574 and PTA 2575; deposited with the ATCC on January 5, 2001, and having depositor reference numbers TS-1, TS-2, AC-1, and AC-2; and/or as set forth, for example, in Table 1A, 6 and 7). The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. Further, techniques known in the art can be used to verify the nucleotide sequences of SEQ ID NO:X.

[58] The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

RACE Protocol For Recovery of Full-Length Genes

[59] Partial cDNA clones can be made full-length by utilizing the rapid amplification of cDNA ends (RACE) procedure described in Frohman, M.A., et al., Proc. Nat'l. Acad.

Sci. USA, 85:8998-9002 (1988). A cDNA clone missing either the 5' or 3' end can be reconstructed to include the absent base pairs extending to the translational start or stop codon, respectively. In some cases, cDNAs are missing the start codon of translation, therefor. The following briefly describes a modification of this original 5' RACE procedure. Poly A⁺ or total RNA is reverse transcribed with Superscript II (Gibco/BRL) and an antisense or complementary primer specific to the cDNA sequence. The primer is removed from the reaction with a Microcon Concentrator (Amicon). The first-strand cDNA is then tailed with dATP and terminal deoxynucleotide transferase (Gibco/BRL). Thus, an anchor sequence is produced which is needed for PCR amplification. The second strand is synthesized from the dA-tail in PCR buffer, Taq DNA polymerase (Perkin-Elmer Cetus), an oligo-dT primer containing three adjacent restriction sites (XhoI, SalI and ClaI) at the 5' end and a primer containing just these restriction sites. This double-stranded cDNA is PCR amplified for 40 cycles with the same primers as well as a nested cDNA-specific antisense primer. The PCR products are size-separated on an ethidium bromide-agarose gel and the region of gel containing cDNA products the predicted size of missing protein-coding DNA is removed. cDNA is purified from the agarose with the Magic PCR Prep kit (Promega), restriction digested with XhoI or SalI, and ligated to a plasmid such as pBluescript SKII (Stratagene) at XhoI and EcoRV sites. This DNA is transformed into bacteria and the plasmid clones sequenced to identify the correct protein-coding inserts. Correct 5' ends are confirmed by comparing this sequence with the putatively identified homologue and overlap with the partial cDNA clone. Similar methods known in the art and/or commercial kits are used to amplify and recover 3' ends.

[60] Several quality-controlled kits are commercially available for purchase. Similar reagents and methods to those above are supplied in kit form from Gibco/BRL for both 5' and 3' RACE for recovery of full length genes. A second kit is available from Clontech which is a modification of a related technique, SLIC (single-stranded ligation to single-stranded cDNA), developed by Dumas et al., *Nucleic Acids Res.*, 19:5227-32 (1991). The major differences in procedure are that the RNA is alkaline hydrolyzed after reverse transcription and RNA ligase is used to join a restriction site-containing anchor primer to the first-strand cDNA. This obviates the necessity for the dA-tailing reaction which results in a polyT stretch that is difficult to sequence past.

[61] An alternative to generating 5' or 3' cDNA from RNA is to use cDNA library double-stranded DNA. An asymmetric PCR-amplified antisense cDNA strand is

synthesized with an antisense cDNA-specific primer and a plasmid-anchored primer. These primers are removed and a symmetric PCR reaction is performed with a nested cDNA-specific antisense primer and the plasmid-anchored primer.

RNA Ligase Protocol For Generating The 5' or 3' End Sequences To Obtain Full Length Genes

[62] Once a gene of interest is identified, several methods are available for the identification of the 5' or 3' portions of the gene which may not be present in the original cDNA plasmid. These methods include, but are not limited to, filter probing, clone enrichment using specific probes and protocols similar and identical to 5' and 3' RACE. While the full length gene may be present in the library and can be identified by probing, a useful method for generating the 5' or 3' end is to use the existing sequence information from the original cDNA to generate the missing information. A method similar to 5' RACE is available for generating the missing 5' end of a desired full-length gene. (This method was published by Fromont-Racine et al., *Nucleic Acids Res.*, 21(7):1683-1684 (1993)). Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcript and a primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest, is used to PCR amplify the 5' portion of the desired full length gene which may then be sequenced and used to generate the full length gene. This method starts with total RNA isolated from the desired source, poly A RNA may be used but is not a prerequisite for this procedure. The RNA preparation may then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase if used is then inactivated and the RNA is treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase. This modified RNA preparation can then be used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction can then be used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the relevant gene.

[63] The present invention also relates to vectors or plasmids which include such DNA sequences, as well as the use of the DNA sequences. The material deposited with the ATCC (deposited with the ATCC on October 5, 2000, and receiving ATCC designation numbers PTA 2574 and PTA 2575; deposited with the ATCC on January 5, 2001, and receiving ATCC designation numbers TS-1, TS-2, AC-1, and AC-2; and/or as set forth, for example, in Table 1A, Table 6, or Table 7) is a mixture of cDNA clones derived from a variety of human tissue and cloned in either a plasmid vector or a phage vector, as described, for example, in Table 7. These deposits are referred to as "the deposits" herein. The tissues from which some of the clones were derived are listed in Table 7, and the vector in which the corresponding cDNA is contained is also indicated in Table 7. The deposited material includes cDNA clones corresponding to SEQ ID NO:X described, for example, in Table 1A (Clone ID NO:Z). A clone which is isolatable from the ATCC Deposits by use of a sequence listed as SEQ ID NO:X, may include the entire coding region of a human gene or in other cases such clone may include a substantial portion of the coding region of a human gene. Furthermore, although the sequence listing may in some instances list only a portion of the DNA sequence in a clone included in the ATCC Deposits, it is well within the ability of one skilled in the art to sequence the DNA included in a clone contained in the ATCC Deposits by use of a sequence (or portion thereof) described in, for example Tables 1A or 2 by procedures hereinafter further described, and others apparent to those skilled in the art.

[64] Also provided in Table 7 is the name of the vector which contains the cDNA clone. Each vector is routinely used in the art. The following additional information is provided for convenience.

[65] Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128, 256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., *Nucleic Acids Res.* 16:7583-7600 (1988); Alting-Mees, M. A. and Short, J. M., *Nucleic Acids Res.* 17:9494 (1989)) and pBK (Alting-Mees, M. A. et al., *Strategies* 5:58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Phagemid pBS may be excised from the Lambda Zap and Uni-Zap XR vectors, and phagemid pBK may be excised from the Zap Express vector. Both phagemids may be transformed into *E. coli* strain XL-1 Blue, also available from Stratagene.

[66] Vectors pSport1, pCMVSPORT 1.0, pCMVSPORT 2.0 and pCMVSPORT 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, also available from Life Technologies. See, for instance, Gruber, C. E., et al., *Focus* 15:59- (1993). Vector lacmid BA (Bento Soares, Columbia University, New York, NY) contains an ampicillin resistance gene and can be transformed into *E. coli* strain XL-1 Blue. Vector pCR[®]2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, available from Life Technologies. See, for instance, Clark, J. M., *Nuc. Acids Res.* 16:9677-9686 (1988) and Mead, D. et al., *Bio/Technology* 9: (1991).

[67] The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, and/or the deposited clone (Clone ID NO:Z). The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

[68] Also provided in the present invention are allelic variants, orthologs, and/or species homologs. Procedures known in the art can be used to obtain full-length genes, allelic variants, splice variants, full-length coding portions, orthologs, and/or species homologs of genes corresponding to SEQ ID NO:X or the complement thereof, polypeptides encoded by genes corresponding to SEQ ID NO:X or the complement thereof, and/or the cDNA contained in Clone ID NO:Z, using information from the sequences disclosed herein or the clones deposited with the ATCC. For example, allelic variants and/or species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for allelic variants and/or the desired homologue.

[69] The polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

[70] The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below). It is often

advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.

[71] The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified using techniques described herein or otherwise known in the art, such as, for example, by the one-step method described in Smith and Johnson, *Gene* 67:31-40 (1988). Polypeptides of the invention also can be purified from natural, synthetic or recombinant sources using techniques described herein or otherwise known in the art, such as, for example, antibodies of the invention raised against the polypeptides of the present invention in methods which are well known in the art.

[72] The present invention provides a polynucleotide comprising, or alternatively consisting of, the nucleic acid sequence of SEQ ID NO:X, and/or the cDNA sequence contained in Clone ID NO:Z. The present invention also provides a polypeptide comprising, or alternatively, consisting of, the polypeptide sequence of SEQ ID NO:Y, a polypeptide encoded by SEQ ID NO:X or a complement thereof, a polypeptide encoded by the cDNA contained in Clone ID NO:Z, and/or the polypeptide sequence encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B. Polynucleotides encoding a polypeptide comprising, or alternatively consisting of the polypeptide sequence of SEQ ID NO:Y, a polypeptide encoded by SEQ ID NO:X, a polypeptide encoded by the cDNA contained in Clone ID NO:Z, and/or a polypeptide sequence encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B are also encompassed by the invention. The present invention further encompasses a polynucleotide comprising, or alternatively consisting of, the complement of the nucleic acid sequence of SEQ ID NO:X, a nucleic acid sequence encoding a polypeptide encoded by the complement of the nucleic acid sequence of SEQ ID NO:X, and/or the cDNA contained in Clone ID NO:Z.

[73] Moreover, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in Table 1B column 6, or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in Table 1B column 6, or any

combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table 1B, column 6, and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table 1B, column 6, and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table 1B, column 6, and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

[74] Further, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1), or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1), or any combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1) and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1) and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated

in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1) and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

[75] Further, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2), or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2), or any combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2) and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2) and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2) and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (See Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.